

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2002, 09:31:20 ; Search time 34.04 Seconds

(without alignments)
1598.888 Million cell updates/sec

Title: US-09-902-713B-96

Perfect score: 2605
Sequence: 1 MRPAFALCLIMQALWPGPG.....LDRFAEGALLAESPLGSSDA 490

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database: A.Geneset.032802.*

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21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2605	100.0	490	20	AA13360
2	2605	100.0	490	21	AAB33460
3	2605	100.0	490	21	AAB24403
4	2605	100.0	490	21	AAU95016
5	2605	100.0	490	22	AAU12349
6	2605	100.0	490	22	AAE06596
7	2230	185.6	428	22	AAB80228
8	1852	63.4	344	21	AA191410
9	1639.5	62.9	331	21	AAB41847
10	802.5	30.8	189	21	AAU91349
11	754.5	29.0	175	21	AAU95031

12	630	24.2	123	21	AAU91409	Human secreted pro
13	336.5	12.9	492	22	AAE05343	Mouse tumor endo
14	307	11.8	492	22	AAU9879	Amino acid sequenc
15	307	11.8	652	21	AAU32345	Human cell surface
16	303	11.6	637	21	AAU32346	Mouse cell surface
17	303	11.6	644	21	AAU79186	Haematopoietic ste
18	303	11.6	644	21	AAU79193	Human urinary thro
19	228	8.8	575	13	AAU20639	Thrombomodulin ana
20	227	8.7	461	15	AAU45335	Thrombomodulin ana
21	227	8.7	462	15	AAU45336	Thrombomodulin ana
22	227	8.7	462	15	AAU45337	Thrombomodulin ana
23	227	8.7	462	15	AAU45338	Thrombomodulin ana
24	227	8.7	462	15	AAU45339	Thrombomodulin ana
25	227	8.7	462	15	AAU45341	Thrombomodulin ana
26	227	8.7	462	15	AAU45342	Thrombomodulin ana
27	227	8.7	462	15	AAU45343	Thrombomodulin ana
28	227	8.7	462	15	AAU45344	Thrombomodulin ana
29	227	8.7	462	15	AAU45346	Thrombomodulin ana
30	227	8.7	462	15	AAU45347	Thrombomodulin ana
31	227	8.7	462	15	AAU45348	Thrombomodulin ana
32	227	8.7	462	15	AAU45349	Thrombomodulin ana
33	227	8.7	462	15	AAU45350	Thrombomodulin ana
34	227	8.7	462	15	AAU45353	Thrombomodulin ana
35	227	8.7	462	15	AAU45354	Thrombomodulin ana
36	227	8.7	462	15	AAU45355	Thrombomodulin ana
37	227	8.7	463	15	AAU45340	Thrombomodulin ana
38	227	8.7	475	13	AAU2032	Truncated human ur
39	227	8.7	476	16	AAU78725	Mature thrombomodu
40	227	8.7	476	16	AAU86377	Modified thrombomo
41	227	8.7	476	16	AAU86376	Modified thrombomo
42	227	8.7	480	13	AAU22013	Truncated human th
43	227	8.7	494	13	AAU24400	Recombinant thromb
44	227	8.7	494	16	AAU78726	Thrombomodulin wit
45	227	8.7	494	16	AAU78727	Thrombomodulin wit

ALIGNMENTS

RESULT	1
AAU13360	standard; Protein; 490 AA.
ID	AAU13360
AC	AAU13360
DT	25-JUN-1999 (first entry)
XX	
DE	Amino acid sequence of protein PRO269.
XX	
KW	Secreted protein; transmembrane protein; human; enterocollitis;
KW	Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW	congenital microvillus atrophy; skin disease; cell growth;
KW	abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW	Parkinson's disease; Alzheimer's disease; AIDS; neuropathy;
KW	fibromodulin; dermal scarring; Usher Syndrome; Atrophla areata;
KW	anti-thrombotic; wound healing; tissue repair.
XX	
OS	Homo sapiens.
XX	
PN	WO914328-A2.
XX	
PD	25-MAR-1999.
XX	
PF	16-SEP-1998; 98WO-US19330.
XX	
PR	25-NOV-1997; 97US-0066840.
PR	17-SEP-1997; 97US-0059113.
PR	17-SEP-1997; 97US-0059115.
PR	17-SEP-1997; 97US-0059117.
PR	17-SEP-1997; 97US-0059119.
PR	17-SEP-1997; 97US-0059121.
PR	17-SEP-1997; 97US-0059122.
PR	17-SEP-1997; 97US-0059184.

18-SEP-1997; 97US-0059263.
 PR 18-SEP-1997; 97US-0059266.
 PR 15-OCT-1997; 97US-0062125.
 PR 17-OCT-1997; 97US-0063285.
 PR 17-OCT-1997; 97US-0063287.
 PR 21-OCT-1997; 97US-0063486.
 PR 24-OCT-1997; 97US-0062814.
 PR 24-OCT-1997; 97US-0062816.
 PR 24-OCT-1997; 97US-0063045.
 PR 24-OCT-1997; 97US-0063120.
 PR 24-OCT-1997; 97US-0063121.
 PR 24-OCT-1997; 97US-0063122.
 PR 27-OCT-1997; 97US-0063128.
 PR 27-OCT-1997; 97US-0063329.
 PR 28-OCT-1997; 97US-0063327.
 PR 28-OCT-1997; 97US-0063541.
 PR 28-OCT-1997; 97US-0063542.
 PR 28-OCT-1997; 97US-0063544.
 PR 28-OCT-1997; 97US-0063549.
 PR 28-OCT-1997; 97US-0063550.
 PR 29-OCT-1997; 97US-0063564.
 PR 29-OCT-1997; 97US-0063435.
 PR 29-OCT-1997; 97US-0063702.
 PR 29-OCT-1997; 97US-0063732.
 PR 29-OCT-1997; 97US-0063738.
 PR 29-OCT-1997; 97US-0063739.
 PR 29-OCT-1997; 97US-0064215.
 PR 31-OCT-1997; 97US-0063870.
 PR 31-OCT-1997; 97US-0064103.
 PR 03-NOV-1997; 97US-0064248.
 PR 07-NOV-1997; 97US-0064809.
 PR 12-NOV-1997; 97US-0065186.
 PR 17-NOV-1997; 97US-0065846.
 PR 18-NOV-1997; 97US-0065693.
 PR 21-NOV-1997; 97US-0066120.
 PR 21-NOV-1997; 97US-0066364.
 PR 24-NOV-1997; 97US-0066772.
 PR 24-NOV-1997; 97US-0066466.
 PR 24-NOV-1997; 97US-0066770.
 PR 24-NOV-1997; 97US-0066511.
 PR 24-NOV-1997; 97US-0066453.
 (GETH) GENENTECH, INC.
 Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
 WPI: 1999-229533/15.
 N-PSDB; AAX52231.
 New isolated human genes and polypeptides used in, e.g. treatment of
 gastrointestinal ulceration
 Claim 12; Fig 36; 520pp; English.

CC therapeutic applications in wound healing and tissue repair; PRO317 can
 CC be used for treating problems of the kidney, uterus, endometrium, blood
 CC vessels, or related tissue, e.g. in the heart of genital tract.
 XX
 SQ Sequence 490 AA;
 Query Match 100.0%; Score 2605; DB 20; Length 490;
 Best Local Similarity 100.0%; Pred. No. 8, 2e-200;
 Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRPAFALCLMOMALWPEPGGEHPADACCSAGCYLSHATMKROAEACILRGCA 60
 DB 1 mrfafalcllwqalmpgpggghpdracccsagcyslshatmkrgaeccilrgca 60
 QY 61 LSTVRAGAEIRAVALLRAGPGGGSKDLLFWALERRSHSTLENPLRGFSWLSDDP 120
 DB 61 lstrvragaelravallrpgpggskdllfwalertrshstlenepirgfswwlsddp 120
 QY 121 GGLSDTLQWVEEPORSCARRCAVLQATGVGPAGMKEMRCHLRANGYLCKYQFVLCF 180
 DB 121 gglstdtlqwveeporscarrcaavlqatgvpgagmkemrchlrangylckyqfvlcf 180
 QY 181 APPRGAASNSTYRAPHOLHSALDFSPCTEVYALCRGOLPISTVCTADETIGARMDKLSG 240
 DB 181 apprgaasnstyrappholhsaldfspctevyalcrgolpistvctadetigarmdkls 240
 QY 241 DVLCPGGRYLRAKCAELPNCIDLDGSPACBACATGEELGKGRSGVNSGEGOPTLGSG 300
 DB 241 dvlcpgrgrylrakcaelpncidldgspacbacatgeelgkgrsgvnsgegoptlgsg 300
 QY 301 VPTRRPATATSPVQRTWPIRVDEKLTPLVPEQDMSVTSIPIPMWGSOSTMSTLQM 360
 DB 301 vptrrpatatspvqrtwpirvdekltpvpeqdmstvtsipipmwgsostmstlqm 360
 QY 361 SLQAEKATITPSSGVYSKFNSTSSATPOADFSSAVFIFVRAVVLIITFTVGL 420
 DB 361 slqaeekatitpssgvyskfnstssatpoadfssavfifvravvliitftvgl 420
 QY 421 VLCTHESPSQPKESMGPEGLSDPEPALGSSASHCTNNGVKVGCDLDRDAEGALL 480
 DB 421 vlcthespsqpkesmgspeglsdpepalgssashctnngvkvgcdldrdaegall 480
 QY 481 AESPLGSSDA 490
 DB 481 aesplgssda 490
 RESULT 2
 AAB33460
 ID AAB33460 standard; Protein; 490 AA.
 XX
 AC AAB33460;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO269 protein UNQ236 SEQ ID NO:233.
 XX
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antidiabetic; antidiabetic; neuroprotective;
 KW antianemic; hepatocytic; virucide; antipsoriatic; antiallergic;
 KW antiautomatic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; immune-mediated;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.
 XX

OS Homo sapiens
 XX WO200053758-A2
 XX 14-SEP-2000
 PD 02-MAR-2000; 2000WO-US05841
 XX 08-MAR-1999; 99WO-US05028
 XX 10-MAR-1999; 99US-0123618
 PR 12-MAR-1999; 99US-0123957
 PR 23-MAR-1999; 99US-0125775
 PR 12-APR-1999; 99US-0128849
 PR 20-APR-1999; 99WO-US08615
 PR 28-APR-1999; 99US-0131445
 PR 04-MAY-1999; 99US-0132371
 PR 14-MAY-1999; 99US-0134287
 PR 02-JUN-1999; 99WO-US12252
 PR 23-JUN-1999; 99US-0141037
 PR 20-JUL-1999; 99US-0144758
 PR 06-JUL-1999; 99US-0145698
 PR 08-JUL-1999; 99US-0146222
 PR 01-SEP-1999; 99WO-US20111
 PR 08-SEP-1999; 99WO-US20594
 PR 13-SEP-1999; 99WO-US20944
 PR 15-SEP-1999; 99WO-US21090
 PR 15-SEP-1999; 99WO-US21547
 PR 05-OCT-1999; 99WO-US23089
 PR 29-OCT-1999; 99US-0162506
 PR 29-NOV-1999; 99WO-US28214
 PR 30-NOV-1999; 99WO-US28313
 PR 30-NOV-1999; 99WO-US28409
 PR 01-DEC-1999; 99WO-US28301
 PR 01-DEC-1999; 99WO-US28634
 PR 02-DEC-1999; 99WO-US28551
 PR 02-DEC-1999; 99WO-US28564
 PR 16-DEC-1999; 99WO-US30095
 PR 20-DEC-1999; 99WO-US30099
 PR 30-DEC-1999; 99WO-US31274
 PR 05-JAN-2000; 2000WO-US00219
 PR 06-JAN-2000; 2000WO-US00277
 PR 06-JAN-2000; 2000WO-US00376
 PR 11-FEB-2000; 2000WO-US03565
 PR 18-FEB-2000; 2000WO-US04341
 PR 18-FEB-2000; 2000WO-US04342
 PR 22-FEB-2000; 2000WO-US04414
 XX
 PA (GENTH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WT, Yan M;
 XX
 DR WPI: 2000-572271/53.
 N-PSDB; AAC58625.
 XX
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 XX arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
 XX
 PS Claim 33; Fig 94; 309pp; English.
 XX
 CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central

CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 490 AA:
 Query Match 100.0%; Score 2605; DB 21; Length 490;
 Best Local Similarity 100.0%; Pred. No. 8.2e-200;
 Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 mrfafalclllwqalwpgpggghptdragsasgacysilhatmkrrgaeeacillrga 60
 QY 61 LSTVRAGAEALRAVLADLRAGPGGSGKDLFWALERRRSHCTLENEPLRGFSWLSDP 120
 DB 61 lstrvagaelravallirgpgpggskdlfwalerrrrshctlenepirgfswlssdp 120
 QY 121 GGLSEDTLQWVEEPORSCFARRCAVLQATGVPEAGKEMRCHLRANGYLCKYQFEVLCP 180
 DB 121 gglseddlqweepqrscfarrcaavlqatgvpeagkewmrchlrangylckyqfevlcp 180
 QY 181 ARPPGASNLSTYRAPQLHSALDFSPPTGVSAFCRGQLPISVYTIADIEGARMKLSG 240
 DB 181 arppgaasnlsyrapqlhsaaldfspptgvsaalcrqglpislvtladelgarwklsg 240
 QY 241 DVLPCPCGRYLRAGCAEPLNCLDLCGFAECATGFEELGKDGKSCVTSGEQPTLGATG 300
 DB 241 dvlpcpcgrylragsaeplnclldlcfacatgfeelgkdgkscvtsgeqptlgatg 300
 QY 301 VPTRRPAPATSPVORTWPIRYDEKLGEPPLVPEODNSVTSIPELPRNGSOSTMSTLM 360
 DB 301 vptrrpapatspvortwpirydeklgetplvpeodnsvtsipeiprngsostmstlqm 360
 QY 361 SIQAESKATITPSSGVISFENSTTSATPOAPSSAAVFIFPSTVAVVLTITMVLGL 420
 DB 361 siqaeskatitpssgvvisfnsttsatpaoapssaaavfifpstaavvltitmvlg 420
 QY 421 VKLCEHESPSSQPRKESMGPGLIESDPEPALGSSSAHCTNNGVKGGCDLDRADGALL 480
 DB 421 vklcfhespsqprkesmmpgliesdpepalgssahctnngvkvggcdldirdagall 480
 QY 481 AESPLGSSDA 490
 DB 481 aesplgssda 490
 RESULT 3
 AAB24403 standard; Protein; 490 AA.
 ID AAB24403
 AC AAB24403;
 XX 07-NOV-2000 (first entry)
 DE Human PRO269 protein sequence SEQ ID NO:77.
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
 KW cytotatic; gene therapy; vaccine.
 OS Homo sapiens.
 XX WO200032221-A2.
 PN

PD 08-JUN-2000
 XX 30-NOV-1999; 99WO-US28313.
 XX 01-DEC-1998; 98WO-US25108.
 PR 16-DEC-1998; 98US-0112850.
 PR 12-JAN-1999; 99US-0115554.
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 XX (GENTECH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A,
 PI Godowski PJ, Gurney AL, Klein RD, Kuoni SS, Paoni NF, Smith V,
 PI Watanabe CK, Williams PM, Wood WI,
 DR WPI; 2000-412154/35.
 DR N-PSDB; AAA77570.
 XX Nucleic acids encoding PRO polypeptides useful for preventing,
 PT diagnosing and treating disorders in mammals
 PT angiogenic disorders in mammals
 XX Claim 72; Fig 32; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating disorders in mammals
 CC cardiovascular, endothelial or angiogenic disorder in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularization,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate PRO expression such as cardiovascular, endothelial or
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
 CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
 CC containing them and the PRO polypeptide may be used to treat disorders
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
 CC the exemplification of the present invention.

XX Sequence 490 AA:

Query Match 100.0%; Score 2605; DB 21; Length 490;
 Best Local Similarity 100.0%; Pred. No. 812e-200;
 Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPALCLIMQALWPGGGGHHPTADRAAGSASACSLHHAHMKROAEACTLRGCA 60
 DB 1 mpataclclwqalwpggggghptadragcsasgacyslhahmkrgaaeactlrgga 60
 QY 1 ISTRVAGELRAVLALLRAGPGPGGSKDLFWALERRHCHLENNPLRGFMSLSDP 120
 DB 61 lstrvageelravallalragpgpggskdlflwalerrhchleenneplrgfmslssdp 120
 QY 121 GLESDTLQWMEERQSTARCACAVLATGSEVAPGKEMKCHLRANGYLCKYFVLCIP 180
 DB 121 glesdltlqwmeerqstarcacavlatgsevapgkemmchlrangylckyfevlc 180
 QY 181 APRGAASNLSTYRAPFOLHSAALDFSPGTEVSALCRGOLPISTCTIADETGARWDLKLG 240

DB 181 aprgaasnlstyrapfolsaaldspgtesalscrgolpistctiadetgarwcklsg 240
 QY 241 DYLCPCGRTLRACKCAELPNCIDDLGFAECATGELKDKRSCVTSGEQPTLGATG 300
 DB 241 dylcpccgrtllrckcaelpnciddlgfaccatgelfgkdkrscvtsgeqptlgatg 300
 QY 301 VPTRRPATATSPVPOETWPIRYDEKIGERPLVPEQDNSTYSIPEIRNGSOSTMTLOM 360
 DB 301 vptrrpatatspvpoetwpirydekigerplvpeqdnstysipeirngsostmtlqm 360
 QY 361 SLOAESKATTPSGSVLSKENTSSATPOAFDSSAVVEIFSPVAVVLTITMTVGLT 420
 DB 361 slqaeskattppsgsvlskntssatpofdssavveifspvavvltitmtvgtl 420
 QY 421 VKLCFHESPSSOPRKESKMPGLESPEDEPAALGSSAHCTNNGVKVGCDLDRRAEAL 480
 DB 421 vkcfhespsoprkessmpglespepeaalgssahctnngvkvgcdldrraeal 480
 QY 481 AESPLGSSDA 490
 DB 481 aesplgssda 490

RESULT 4
 ID AAY95016
 ID AAY95016 standard; Protein; 490 AA.

XX AAY95016;

DT 19-JUN-2000 (first entry)

DE Human secreted protein vp15_1, SEQ ID NO:72.

KM Human; secreted protein; cancer; tumour; cardiovascular disorder;
 KM blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
 KM infection; fungal; bacterial; viral; HIV; allergy; arthritis;
 KM neurodegenerative disease; asthma; contraceptive.

OS Homo sapiens.

PM WO200011015-A1.

PD 02-MAR-2000.

PF 24-AUG-1999; 99WO-US19351.

PR 24-AUG-1998; 98US-0097638.

PR 24-AUG-1998; 98US-0097659.

PR 09-SEP-1998; 98US-0099618.

PR 28-SEP-1998; 98US-0102092.

PR 25-NOV-1998; 98US-0109978.

PR 23-DEC-1998; 98US-0113645.

PR 23-DEC-1998; 98US-0113646.

PR 23-AUG-1999; 99US-0379246.

PA (ALPH-) ALPHAGENE INC.

PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

DR WPI; 2000-224657/19.

PT New secreted or transmembrane proteins and polynucleotides encoding
 PT them, useful for treating neurodegenerative disorders, autoimmune
 PT diseases and cancer

PS Claim 81, Page 331-332; 357pp; English.
 CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
 CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
 CC proteins of the invention include those that are thought to be only
 CC partially secreted, i.e., transmembrane proteins. The proteins of the
 CC invention may exhibit one or more activities selected from the following:

CC cytokine activity; cell proliferation; differentiation; immune
 CC modulation; haematopoiesis; regulation; tissue growth activity;
 CC activin/inhibin activity; chemotactic/chemokine activity; haemostatic
 CC and thrombolytic activity; anti-inflammatory activity; and tumour
 CC inhibition activity. The proteins may be administered to patients as
 CC vaccines, and the nucleotides may be used as part of a gene therapy
 CC regime. Diseases or conditions that may be treated using the proteins or
 CC nucleotides of the invention include autoimmune diseases; genetic
 CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
 CC fungal and viral infections, especially HIV; multiple sclerosis;
 CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
 CC insulin dependent diabetes mellitus; and allergic reactions such as
 CC asthma and anaemia. They may also be used for treating wounds, burns,
 CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease and amyotrophic
 CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may
 CC additionally be useful as contraceptives. Nucleic acid sequences of the
 CC invention may be used in chromosome mapping, and as a source of
 CC diagnostic primers and probes. The present sequence represents one of the
 CC 40 proteins of the invention.

Sequence 490 AA:

Query Match 100.0%; Score 2605; DB 21; Length 490;
 Best Local Similarity 100.0%; Pred. No. 8.2e-200;
 Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPAFLCLLMQALMPGSGEHPADRACSGAGCYSLHHTMKRQAEEACILGGA 60
 Db 1 mrfafclllwglwlpypggsgelptdragscsagcyslhhtmkrgaeeacilgga 60
 QY 61 LSTVRAAEIRAVLALLRAGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSDDP 120
 Db 61 lstrvraaeliravllallragpggskdllfwvalerrshctleneplrgfswlsddp 120
 QY 121 GGESEDTLQWVEREORSCRRARCAVQATGCVDPAGMKERCHLRANGYLCCKQFEVLCF 180
 Db 121 ggeledtlqwevepqrscarravqatgcvdpagmkemrchlrangylckkyfevlcp 180
 QY 181 APRPGAASNLSTYRAPFQLSHALDFSPGTEVVALCRGQPIVTCFADIGARMDLSC 240
 Db 181 apprgaasnlsyrapfqlshaaldfspgtevalcrqgipivtcfadigarwdlsc 240
 QY 241 DVLCPCGRYLRAGKCAELPNCDDLGCFACGATGFELEKDRSCVTSGEQPTLGATG 300
 Db 241 dvlpcpgrylragkcaelpncddlgcfacgatgfelekdgrscvtsgeqptlgatg 300
 QY 301 VPTRRPRTATSPVPORTMPIRVDEKLGEPVLPEDQNSTSTIPEIPRMGSOSTMSTLQM 360
 Db 301 vptrrpataispvprtwpirvdeklgepvlpedqnsststipeiprmgsostmstlqm 360
 QY 361 SLQAEKATITPGSVYSKFNSTSSATPAQFSSSAVVIFSTAVVVLITMTVLGL 420
 Db 361 slgaekatitpgsvyskfnstssatpafsssaavvifstavvvlitmtvlgl 420
 QY 421 VKICFHESSSQPRKESMGPGLESDEPAALGSSSAHCTNNCKVQDCDLRRAEGLAL 480
 Db 421 vkicfhespsqprkesmgpglesdepaalgsssahtcnnckvqdcclrdraegall 480
 QY 481 AESSPGSSDA 490
 Db 481 aesspgssda 490

RESULT 5

AAU12349 standard: Protein: 490 AA.

XX AAU12349;
 XX 24-OCT-2001 (first entry)
 DT XX
 XX

DE Human PRO269 polypeptide sequence.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIa; gene therapy.

OS Homo sapiens.

PN MO200140466-A2.

XX 07-JUN-2001.

PF 01-DEC-2000; 2000WO-US32678.

XX 01-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US31243.

PR 06-JAN-2000; 2000WO-US00277.

PR 11-FEB-2000; 2000WO-US00376.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.

PR 01-MAR-2000; 2000WO-US05601.

PR 20-MAR-2000; 2000WO-US07377.

PR 21-MAR-2000; 2000WO-US07532.

PR 30-MAR-2000; 2000WO-US08439.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 10-NOV-2000; 2000WO-US30873.

(GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

DR WPI: 2001-408281/43.

DR N-PSDB; AAS21421.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect

PT other PRO polypeptides, link bioactive molecules to cells expressing

PT PRO polypeptides, and detect the presence of mammalian tumours e.g.

PT lung, breast, prostate, cervical

XX Claim 12; Fig 356; 813pp; English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of

CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.

XX Sequence 490 AA:

Query Match Best Local Similarity 100.0%; Score 2605; DB 22; Length 490;
 Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPAFLCLIMOLMPGSGGGEHPADRAGCSASAGCSLSHATMKRQAAEACILRGA 60
 Db 1 mrpafalclimolmpgsgggehpadragcsasagcslshtmkrgaaeacilryga 60
 QY 61 LSTVRAGAEALAVALLRAGPGGSGKDLFWALERRSHCTLENPLRGFWSLSDP 120
 61 lstrvagaelavallragpggsgkdllfwalerrshctlenplrgfswlsdp 120
 QY 121 GLESDTLQWVEEPPORSTARCAYLOATGVEPAGKEMKCHLRANGYLCKYFVLCP 180
 Db 121 glesdltqwveepgprstarcayloatgvepagkemmchlrrangylckyfevlcp 180
 QY 181 APRGAASNLSTYRAPFOHSAALDFSPGTEVSALCRGOLPISTYCTADEIGARWDLSC 240
 Db 181 aprgaasnlsyrapfghsaaldfspgtevsalcrgolpistycadeigarwdlsg 240
 QY 241 DVLPFCPRYLRAGKCAELPNCIDLGFGNCEATGFELEGDGSCTVSGEGOPTLGCTG 300
 Db 241 dvlpfcprylragkcaelpncidlgfgnceatgfelegdgsctvsggoptlgctg 300
 QY 301 VPTRRPATATSPVORTWPIRVDKLGEMPLEVEQDNSTVSIPEIRMGOSMTMTOM 360
 Db 301 vptrrpatatspvortwpirvdkgempleveqdnstvsipeirmgosmtmtom 360
 QY 361 SLOESKATTPGSGSVSKRNSTTSSATPAFDSASNVFIYSTAVVLLMTVLGL 420
 Db 361 slgeskattpgsgsvskrnsttssatpafdsasnfvfiystavvllmtvlg 420
 QY 421 VKLGFHSPSSOPRKESMGPGLSDPEPALGSSSAHCTNNGVKVDCLRRABGALL 480
 Db 421 vklgfhspsoprkesmgpplsdpepalgssahctnngvkvdclrrabgall 480
 QY 481 AESPLGSSDA 490
 481 aesplgssda 490

RESULT 6
 ID AAE06596 standard; Protein; 490 AA.

XX AAE06596;
 AC 25-SEP-2001 (first entry)
 DT Human protein having hydrophobic domain, HP03983.
 DE Human: hydrophobic domain; gene therapy; nutritional supplement;
 KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
 KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
 KW haematopoiesis; tissue growth activity; Parkinson's disease; cytoskeletal;
 KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
 KW contraceptive; anti-fertility; anti-inflammatory.
 XX Homo sapiens.
 OS
 XX
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..22

FT Protein /label= signal peptide
 FT 23..490 /note= "Mature human protein with hydrophobic domain"

XX W0200149728-42.

XX 12-JUL-2001.

XX 28-DEC-2000; 2000MO-JP09359.

XX 06-JAN-2000; 2000JP-0000585.

XX 06-JAN-2000; 2000JP-0000588.

XX 11-JAN-2000; 2000JP-0002299.

XX 03-FEB-2000; 2000JP-0026862.

XX 03-MAR-2000; 2000JP-0058367.

XX (PROT-) PROTEGENE INC.

XX (SAGA) SAGAMI CHEM RES CENT.

XX Kato S, Kimura T;

XX WPI, 2001-418355/44.

XX N-PSDB; AADI2591.

XX Human proteins with hydrophobic domains and the nucleic acids encoding
 PT them, useful for preventing diagnosing and treating e.g. cancer,
 PT Alzheimer's and inflammation

XX Claim 1; Page 110-111; 563pp; English.

XX The present sequence is human protein with hydrophobic domain,
 CC HP03983. The polynucleotide and polypeptide of the invention
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The polynucleotides
 CC may be used to produce the polypeptide, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. The
 CC polynucleotides and its complementary sequences may also be used as DNA
 CC probes in diagnostic assays and also used in gene therapy. The
 CC polypeptides may also be used as antigens in the production of antibodies
 CC and in assays to identify modulators of polypeptide expression and
 CC activity. The polypeptides and nucleic acids may be used as nutritional
 CC supplements, to modulate cytokine and cell proliferation activity, to
 CC modulate immune stimulation or suppression (e.g. for the treatment of
 CC microbial infections and autoimmune disorders such as multiple sclerosis,
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
 CC disease), to modulate actinin and inhibit activity (e.g. for controlling
 CC fertility), to modulate chemotactic and chemokinetic activity, to
 CC modulate haemostatic and thrombolytic activity, to modulate receptor
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.

XX Sequence 490 AA:

Query Match Best Local Similarity 100.0%; Score 2605; DB 22; Length 490;
 Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPAFLCLIMOLMPGSGGGEHPADRAGCSASAGCSLSHATMKRQAAEACILRGA 60
 Db 1 mrpafalclimolmpgsgggehpadragcsasagcslshtmkrgaaeacilryga 60
 QY 61 LSTVRAGAEALAVALLRAGPGGSGKDLFWALERRSHCTLENPLRGFWSLSDP 120
 Db 61 lstrvagaelavallragpggsgkdllfwalerrshctlenplrgfswlsdp 120
 QY 121 GLESDTLQWVEEPPORSTARCAYLOATGVEPAGKEMKCHLRANGYLCKYFVLCP 180
 Db 121 glesdltqwveepgprstarcayloatgvepagkemmchlrrangylckyfevlcp 180
 QY 181 APRGAASNLSTYRAPFOHSAALDFSPGTEVSALCRGOLPISTYCTADEIGARWDLSC 240
 181 aprgaasnlsyrapfghsaaldfspgtevsalcrgolpistycadeigarwdlsg 240

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Db 181 aprgaasnllyrapfqlhsaaldfspptevsalcrqqlpistcladeigarkwklsg 240
Qy 241 DVLCPCGRYLRAKCAELPNCIDLDLGFAECATGFEELGKDRSCVTSGEQPTLGCTG 300
Db 241 dvlcpcgrylrakcaelpncidldlgfacedatgfeigkdrscvtsgeqptlgctg 300
Qy 301 VPTRRPATATSPVPORTWPIRYDEKLGEPPLVPEODNSTVSTIPETPRMKSOSTMTSLQM 360
Db 301 vptrrpatatspvportwpiirydekigepplvpeodnstvstipeiprmksostmtslqm 360
Qy 361 SLOAESKATITPSGVSYSKFNSTTSATPOAFDSSSAVVFIFSTAVVVLITMTVLGL 420
Db 361 slgaeskatitpsgvsyskfnsttsatpafidsssaavvifvstavvvlitmtvlgl 420
Qy 421 VKLCFHESSOPRKESMGPPGLESDPEPALGSSSAHCTNNGVKVGDCLDRRAEGALL 480
Db 421 vklcfhessoprkessmgppglesdpepalgsssaahctnngkvvgdclldrraegall 480
Qy 481 AESPLGSSDA 490
Db 481 aesplgssda 490

RESULT 7
AAB80228
ID AAB80228 standard; Protein; 428 AA.
AC AAB80228;
XX
XX 24-APR-2001 (first entry)
DE Human PRO269 protein.
XX
XX Human; PRO; dermatological; antiproliferative; cytostatic; antiinflammatory;
XX antiparkinsonian nootropic; neuroprotective; vulnerary; cardiact;
XX antidiabetic; vasorelaxant; antihypertensive; antihypertensive; cancer;
XX antitumor; antifertility; antidiabetic; antiviral; diabetes;
XX ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
XX ischaemia; inflammation.
XX
XX Homo sapiens.
XX
XX MO200104311-AL.
PN
XX 18-JAN-2001.
PD
XX 22-FEB-2000; 2000MO-US04414.
PF
XX 07-JUL-1999; 99US-0143048.
PI 06-JUL-1999; 99US-0145698.
PI 28-JUL-1999; 99US-0146222.
PR 08-SEP-1999; 99MO-US20594.
PR 13-SEP-1999; 99MO-US20944.
PR 15-SEP-1999; 99MO-US21090.
PR 15-SEP-1999; 99MO-US21547.
PR 05-OCT-1999; 99MO-US23089.
PR 29-NOV-1999; 99MO-US28214.
PR 30-NOV-1999; 99MO-US28313.
PR 16-DEC-1999; 99MO-US30095.
PR 20-DEC-1999; 99MO-US30911.
PR 20-DEC-1999; 99MO-US30999.
PR 05-JAN-2000; 99MO-US00219.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Grimaldi CJ, Gunney AL, Hillan KJ, Kijavits ID;
XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PW, Wood WL;
XX
XX WPI: 2001-081051/09.
XX N-PSDB: AAF72389.

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XX
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT Alzheimer's disease)
XX
XX Claim 1; Fig 36; 393pp; English.
XX
XX The present sequence is one of sixty one novel secreted and
XX transmembrane PRO polypeptides. The PRO polypeptides are
XX useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
XX squamous cell carcinoma), gastrointestinal disorders (e.g.
XX enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
XX Parkinson's disease), wound repair, cardiovascular disorders (e.g.
XX endometrial bleeding, angiogenesis, ischaemia such as coronary
XX ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
XX rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
XX diabetes and retinal disorders such as retinitis pigmentosa.
XX The PRO nucleic acids have applications in molecular biology, including
XX use as hybridization probes, and in chromosome and gene mapping.
XX
XX Sequence 428 AA:

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Query Match 85.6%; Score 2230; DB 22; Length 428;
Best Local Similarity 87.3%; Pred. No. 6; e-170;
Matches 428; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

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Qy 1 MRPAFALCLIMQWPGGEGEPTADACSGACYSIHHMTMKROAEACILIRGA 60
Db 1 mrpafalclimqwpagggeptadacsgacysihhmtmkroaeacilirga 60
Qy 61 LSTVRAGAEIRAVLALLRAPPDGGGSKDLFWALERRRSHCTLENEPRGFSWLSDDP 120
Db 61 lstvragaelravallrappdgggskdlfwalerrrshctleneprgfswlsddp 120
Qy 61 lsvtragaelravallrappdgggskdlfwalerrrshctleneprgfswlsddp 120
Qy 121 GGEESDTLOWVEBPQSCYTRACAVLQATGCVBPAGCKEMKCHLRANGYLCKTQFEVLCP 180
Db 121 ggeesdtlowvebpqscytracavqlatgcvbpagckemkchlrangylcktyfevlcp 180
Qy 121 ggesdtlowvebpqscytracavqlatgcvbpagckemkchlrangylcktyfevlcp 180
Qy 181 APPGAASNLSTYRAPFQLHSAALDFSPGTEVSALCRGQLPISTVCIADEIGARMDLGS 240
Db 181 aprgaasnlstyrapfqlhsaaldfspgtevsalcrgqlpistvciaideigarmdlgs 240
Qy 241 DVLCPCGRYLRAKCAELPNCIDLDLGFAECATGFEELGKDRSCVTSGEQPTLGCTG 300
Db 187 -----rylrqkcaelpncidldlgfacedatgfeigkdrscvtsgeqptlgctg 238
Qy 301 VPTRRPATATSPVPORTWPIRYDEKLGEPPLVPEODNSTVSTIPETPRMKSOSTMTSLQM 360
Db 239 vptrrpatatspvportwpiirydekigepplvpeodnstvstipeiprmksostmtslqm 238
Qy 361 SLOAESKATITPSGVSYSKFNSTTSATPOAFDSSSAVVFIFSTAVVVLITMTVLGL 420
Db 239 slgaeskatitpsgvsyskfnsttsatpafidsssaavvifvstavvvlitmtvlgl 358
Qy 421 VKLCFHESSOPRKESMGPPGLESDPEPALGSSSAHCTNNGVKVGDCLDRRAEGALL 480
Db 359 vklcfhessoprkessmgppglesdpepalgsssaahctnngkvvgdclldrraegall 418
Qy 481 AESPLGSSDA 490
Db 419 aesplgssda 428

RESULT 8
AA91410
ID AA91410 standard; Protein; 344 AA.
XX
XX AA91410;
XX
XX 29-JUN-2000 (first entry)
XX

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Human secreted protein sequence encoded by gene 4 SEQ ID NO:131.

Human; secreted protein; diagnosis; neuroprotective; nootropic;
neuroleptic; anti-infective; cerebroprotective; immunomodulatory;
anti-microbial; cardiac; cytosolic; anti-inflammatory; haemostatic;
anticonvulsant; vasotropic; vaccine; gene therapy; anti-sense therapy;
neural; reproductive; immune disorder; immunodeficiency; infection;
lymphoma; demyelinating disease; autoimmune; cancer; inflammation;
aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disease;
Huntington's disease; Tourette syndrome; multiple sclerosis; meningitis;
ischemia; mania; dementia; obsessive compulsive disorder;
viral prophylaxis; developmental disorder; sexually-linked disorder;
cardiovascular disorder; food additive; preservative; chromosome 14.

Homo sapiens.

MO200011014-A1.

02-MAR-2000.

24-AUG-1999; 99WO-US19330.

25-AUG-1998; 98US-0097917.

31-AUG-1998; 98US-0098634.

(HUMA-) HUMAN GENOME SCI INC.

Moore PA, Riben SM, Olsen HS, Shi Y, Rosen CA, Florence KA;

Soppet DR, Lafleur DW, Endress GA, Ebner R, Komatsoulis G;

Duan RD;

WPI: 2000-224656/19.

Novel secreted proteins and corresponding DNA molecules that can be used to prevent, treat and diagnose disease in humans, for example, Alzheimer's, cancer, and immune disorders.

Disclosure; Page 391-392; 416pp; English.

The polynucleotide sequences given in AAA26281 to AAA26336 encode the human secreted proteins given in AAY91346 to AAY91449. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: neuroprotective; nootropic; neuroleptic; anti-infective; cerebroprotective; immunomodulatory; anti-microbial; cardiac; cytosolic; anti-inflammatory; haemostatic; anticonvulsant; and vasotropic. The polynucleotides and proteins may be used to prevent, treat or ameliorate a medical condition, e.g. by protein or gene therapy. Conditions treatable by the proteins of the invention include neural, reproductive, or immune disorders, especially immunodeficiency, infection, lymphomas, demyelinating diseases, auto-immunities, cancer, general microbial infection, inflammation, aneurysms and haemorrhages. Specific examples include: Alzheimer's disease; Parkinson's; Huntington's; Tourette syndrome; multiple sclerosis; meningitis; ischemia; prostate cancer; mania; dementia; obsessive compulsive disorder and viral prophylaxis. The polynucleotides and proteins can also be used in the detection of disorders associated with the function of the protein, for example, the detection of cardiovascular disorders, sexually-linked disorders, or disorders of the cardiovascular system. They may also be used as food additives or preservatives. AAA26272 to AAA26280 and AAY91345 are sequences used in the exemplification of the present invention.

Sequence 344 AA:

Query Match 63.4%; Score 1652; DB 21; Length 344;

Best Local Similarity 98.1%; Pred. No. 7.9e-124;

Matches 316; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

169 YLCKTQFVLCAPPPGASNTSYRAPQLHSAALDPSPPGTEVSALRGQLPISVTGIA 228

23 YLCKYGFVLCAPPPGASNTSYRAPQLHSAALDPSPPGTEVSALRGQLPISVTGIA 82

QY 229 DEIGARMDKISGDVLCPCPGRYLRAGCAELPNCIDDLGCFACCATGFELGDKGRSCYT 288
DB 83 delgarwdklsgrdlcppepyrlragkcaelpnclddlgcfacccatgfgldgrscvlt 142
QY 289 SGEQPTLGGCVTRRPPATSPVQRTPIRVYDEKLGSETPLVPEQDMSVTISPEIRP 348
DB 143 sgeqptlggcvtrrppatspvqrtpirvydeklgsetplvpeqdmsvtispeirp 202
QY 349 WGSOSTMSTLQMSLQASKATTPPSGSVISKFNSTTSATPOAFDSSAVYFVSTAVY 408
DB 203 wgsostmstlqmslqasakatppsgsviskfnsttsatpofdssavvyfvsavvy 262
QY 409 VLVITMTVIGIVLCHEPSSOPKESGPPLESDEPPALGSSSAHCTNNGVKVD 468
DB 263 vlvitmtvigivlchepssopkesgpplesdeppalgsssaahctnngvkvd 322
QY 469 CDLRRAEGALLAESPLGSSDA 490
DB 323 cdllrreagallaesplgssda 344

RESULT 9

AAA81847

ID ABA41847 standard; Protein; 331 AA.

AAA81847;

08-FEB-2001 (first entry)

Human ORFX ORF1611 polypeptide sequence SEQ ID NO:3222.

Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;
vulnerary; antiparasitic; antiparkinsonian; nootropic; neuroprotective;
anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;
immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
hypotensive; dermatological; immunosuppressive; anti-inflammatory;
antiviral; antibacterial; antifungal; antineoplastic; antihypertoid;
anti-neoplastic; gene therapy; cancer; proliferative disorder; hypertension;
neurodegenerative disorder; osteoarthritis; graft vs host disease;
cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
bone damage; cartilage damage; antiinflammatory disease; coagulation;
thrombosis; contraceptive.

Homo sapiens.

WO200058473-A2.

05-OCT-2000.

31-MAR-2000; 2000WO-US08621.

31-MAR-1999; 99US-0127607.

02-APR-1999; 99US-0127636.

05-APR-1999; 99US-0127728.

30-MAR-2000; 2000US-0540763.

(CURA-) CURAGEN CORP.

Shinkets RA, Teach M;

WPI: 2000-602362/57.

N-PSDB; AAC76056.

Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

Claim 11; Page 2431-2432; 5507pp; English.

AAC74446 to AAC77606 encode the proteins given in ABA40237 to ABA43397;

CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antiproliferative; antiparkinsonian; neuroprotective;
 CC osteoprotective; anticonvulsant; antidiabetic; immunosuppressive;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antidiabetic; antidiabetic; antiviral; antifungal; antineoplastic;
 CC antidiabetic; antidiabetic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy.
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, anti-inflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 331 AA:

Query Match 62.9%; Score 1639.5; DB 21; Length 331;
 Best Local Similarity 97.8%; Pred. No. 7.5e-123;
 Matches 310; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

OY 128 LQWVEPQSCARACAVQATGVEPAPKMKRCHLRANGYCKTQFELCPAPRGAA 187
 DB 15 VQVVEPQSCARACAVQATGVEPAPKMKRCHLRANGYCKTQFELCPAPRGAA 73
 OY 188 SNUSTRAPQLHSALDSPETVESALCRGQLPISVTIADIGARMKLSDVLPCP 247
 DB 74 SNUSTRAPQLHSALDSPETVESALCRGQLPISVTIADIGARMKLSDVLPCP 133
 OY 248 GYVLARCAELPNCIDLDGFCACATGFEKXGRCSCVTSEGGPTLCGTCVPRRRP 307
 DB 134 GYVLARCAELPNCIDLDGFCACATGFEKXGRCSCVTSEGGPTLCGTCVPRRRP 193
 OY 308 AATSPVPORTPIRDEKIGETPLVEPDNSVTSIPETPRMCSOSTMGLQMSIAESK 367
 DB 194 AATSPVPORTPIRDEKIGETPLVEPDNSVTSIPETPRMCSOSTMGLQMSIAESK 253
 OY 368 AATSPVPORTPIRDEKIGETPLVEPDNSVTSIPETPRMCSOSTMGLQMSIAESK 427
 DB 254 AATSPVPORTPIRDEKIGETPLVEPDNSVTSIPETPRMCSOSTMGLQMSIAESK 313
 OY 428 SPSQPRKESMGPGGLE 444
 DB 314 SPSQPRKESMGPGGLE 330

RESULT 10

AAV91349 standard: Protein; 189 AA.

AAV91349;

29-JUN-2000 (first entry)

Human secreted protein sequence encoded by gene 4 SEQ ID NO:70.

XX Human; secreted protein; diagnosis; neuroprotective; nootropic;
 KW neuroleptic; antianemic; cerebroprotective; immunomodulatory;
 KW anti-microbial; cardiant; cytostatic; anti-inflammatory; haemostatic;
 KW anticonvulsant; vasotropic; vaccine; gene therapy; anti-sense therapy;
 KW neural; reproductive; immune disorder; immunodeficiency; infection;
 KW lymphoma; demyelinating disease; autoimmune; cancer; inflammation;
 KW Huntington's disease; Alzheimer's disease; Parkinson's disease;
 KW ischaemia; mania; dementia; obsessive compulsive disorder;
 KW viral prophylaxis; developmental disorder; sexually-linked disorder;

KW cardiovascular disorder; food additive; preservative; chromosome 14.

XX Homo sapiens.

XX MO200011014-A1.

XX 02-MAR-2000.

XX 24-AUG-1999; 99WO-US19330.

XX 25-AUG-1998; 98US-0097917.

XX 31-AUG-1998; 98US-0098634.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Moore PA, Ruben SM, Olsen HS, Shi Y, Rosen CA, Florence KA;

XX Soppet DR, Lafleur DW, Endress GA, Ehner R, Komatsu G;

XX Duan RD;

XX WPI; 2000-224656/19.

XX N-PSDB; AAA26284.

XX Novel secreted proteins and corresponding DNA molecules that can be

XX used to prevent, treat and diagnose disease in humans, for example,

XX Alzheimer's, cancer, and immune disorders -

XX Claim 11; Page 357; 416pp; English.

The polynucleotide sequences given in AAA26281 to AAA26336 encode the
 human secreted proteins given in AAV91346 to AAV91449. The human secreted
 proteins can have activities based on the tissues and cells they are
 expressed in. Examples of the activities are: neuroprotective; nootropic;
 CC neuroleptic; antianemic; cerebroprotective; immunomodulatory;
 CC anti-microbial; cardiant; cytostatic; anti-inflammatory; haemostatic;
 CC anticonvulsant; and vasotropic. The polynucleotides and proteins may be
 CC used to prevent, treat or ameliorate a medical condition, e.g. by protein
 CC or gene therapy. Conditions treatable by the proteins of the invention
 CC include neural, reproductive, or immune disorders, especially
 CC immunodeficiency, infection, lymphomas, demyelinating diseases,
 CC auto-immunities, cancer, general microbial infection, inflammation,
 CC neurosclerosis and haemorrhages. Specific examples include: Alzheimer's
 CC disease; Parkinson's; Huntington's; Tourette syndrome; multiple
 CC sclerosis; meningitis; ischaemia; prostate cancer; mania; dementia;
 CC obsessive compulsive disorder and viral prophylaxis. The polynucleotides
 CC and proteins can also be used in the detection of disorders associated
 CC with the function of the protein, for example, the detection of
 CC developmental disorders, sexually-linked disorders, or disorders of the
 CC cardiovascular system. They may also be used as food additives or
 CC preservatives. AAA26272 to AAA26280 and AAV91345 are sequences used in
 CC the exemplification of the present invention.

XX Sequence 189 AA:

Query Match 30.8%; Score 802.5; DB 21; Length 189;

Best Local Similarity 84.4%; Pred. No. 2.9e-56;

Matches 157; Conservative 0; Mismatches 26; Indels 3; Gaps 2;

OY 1 MRPAFLCLLMQALWPGGGEHPADBRAGCSASGACYSLHHTMCKROAEACILRGGA 60
 DB 1 MRPAFLCLLMQALWPGGGEHPADBRAGCSASGACYSLHHTMCKROAEACILRGGA 60
 OY 61 LSTVRAGAEIRAVALLLRAGPGGGSKDLFWVALERRRSHCTLENEPLRGFSWLSDP 120
 DB 61 LSTVRAGAEIRAVALLLRAGPGGGSKDLFWVALERRRSHCTLENEPLRGFSWLSDP 120
 OY 121 GGLSTLQWVEPQSCARACAVQATGVEPAPKMKRCHLRANGYCKTQFELCPAPRG 178
 DB 121 GGLSTLQWVEPQSCARACAVQATGVEPAPKMKRCHLRANGYCKTQFELCPAPRG 178
 OY 179 CPAPRG 184
 DB 180 rrapgp 185

RESULT 11
 ID AAY95031 standard; Protein: 175 AA.
 AC AAY95031;
 DT 19-JUN-2000 (first entry)
 DE Human clone vpl5_1 insertional variant ORF SEQ ID NO:131.
 KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
 KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
 KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
 KW neurodegenerative disease; asthma; contraceptive; open reading frame;
 ORF; variant.
 OS Homo sapiens.
 MO2000011015-A1.
 PD 02-MAR-2000.
 PF 24-AUG-1999; 99MO-US19331.
 PR 24-AUG-1998; 98US-0097638.
 PR 24-AUG-1998; 98US-0097659.
 PR 09-SEP-1998; 98US-0099618.
 PR 28-SEP-1998; 98US-0102092.
 PR 25-NOV-1998; 98US-0109978.
 PR 23-DEC-1998; 98US-0113645.
 PR 23-DEC-1998; 98US-0113646.
 PR 23-AUG-1999; 99US-0379246.
 PA (ALPH-) ALPHAGEN INC.
 PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapley P;
 DR WPI: 2000-224657/19.
 XX The new secreted or transmembrane proteins and polynucleotides encoding
 PT them, useful for treating neurodegenerative disorders, autoimmune
 PT diseases and cancer.
 PS Disclosure; Page 351; 357pp; English.
 CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
 CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
 CC proteins of the invention include those that are thought to be only
 CC partially secreted, i.e., transmembrane proteins. The proteins of the
 CC invention may exhibit one or more activities selected from the following:
 CC cytokine activity; cell proliferation; differentiation; immune
 CC modulation; hematopoiesis regulation; tissue growth activity;
 CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
 CC and thrombolytic activity; anti-inflammatory activity; and tumour
 CC inhibition activity. The proteins may be administered to patients as
 CC vaccines, and the nucleotides may be used as part of a gene therapy
 CC regime. Diseases of conditions that may be treated using the proteins or
 CC nucleotides of the invention include autoimmune diseases; genetic
 CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
 CC fungal and viral infections; pulmonary inflammation; Guillain-Barre syndrome;
 CC rheumatoid arthritis; diabetes mellitus; and allergic reactions such as
 CC asthma and anaemia. They may also be used for treating wounds, burns,
 CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease and amyotrophic
 CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may
 CC additionally be useful as contraceptives. Nucleic acid sequences of the
 CC invention may be used in chromosome mapping, and as a source of
 CC diagnostic primers and probes. Sequences AAY95024-Y95025, AAY95029 and
 CC AAY95031-Y95032 represent additional open reading frames (ORFs) that are
 CC encoded by deletion or insertional variants of the cDNA clones of the

CC invention.
 XX Sequence 175 AA;
 SO
 Query Match 29.08; Score 754.5; DB 21; Length 175;
 Best Local Similarity 94.08; Pred. No. 1,8e-52;
 Matches 142; Conservative 2; Mismatches 4; Indels 3; Gaps 1;
 QY 1 MRPAFALCLLMQALMPGGGHEPTADRACSGACYSLHNDKMRQAEACILRGCA 60
 DB 1 mmpafalcilwqalwpgpggheptadragsasgacyslnhnmrgaaecilrrga 60
 QY 61 LSTYRACAEIRAVIALIRAGPGGSKDLFWALERRRSHCTLENEPLRGFSWLSPP 120
 DB 61 lstryracaelravialiragpggskdlfwalerrrshctleneplrgfswlspp 120
 QY 121 GLESDPTLQWEEPORSCTARRCAVLQATGG 151
 DB 121 glesdptlqwweeporsctarrcavlaatgg 148
 RESULT 12
 ID AAY91409 standard; Protein: 123 AA.
 AC AAY91409;
 DT 29-JUN-2000 (first entry)
 DE Human secreted protein sequence encoded by gene 4 SEQ ID NO:130.
 KW Human; secreted protein; diagnosis; neuroprotective; neurotropic;
 KW neuroleptic; antimanic; cerebroprotective; immunomodulatory;
 KW anti-microbial; cardiac; cytosolic; antiinflammatory; haemostatic;
 KW anticonvulsant; vasotropic; vaccine; gene therapy; anti-sense therapy;
 KW neural; reproductive; immune disorder; immunodeficiency; infection;
 KW lymphoma; demyelinating disease; autoimmunity; cancer; inflammation;
 KW aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; Tourette syndrome; multiple sclerosis; meningitis;
 KW ischaemia; mania; dementia; obsessive compulsive disorder;
 KW viral prophylaxis; developmental disorder; sexually-linked disorder;
 KW cardiovascular disorder; food additive; preservative; chromosome 14.
 OS Homo sapiens.
 MO2000011014-A1.
 PD 02-MAR-2000.
 PF 24-AUG-1999; 99MO-US19330.
 PR 25-AUG-1998; 98US-0097917.
 PR 31-AUG-1998; 98US-0098634.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Moore PA, Ruben SM, Olsen HS, Shi Y, Rosen CA, Florence KA;
 PI Soppet DR, Lafleur DW, Endress GA, Ebner R, Komatsoulis G;
 PI Dunn RD;
 DR WPI: 2000-224656/19.
 XX Novel secreted proteins and corresponding DNA molecules that can be
 PT used to prevent, treat and diagnose disease in humans, for example,
 PT Alzheimer's, cancer, and immune disorders.
 PS Disclosure; Page 391; 416pp; English.
 CC The polynucleotide sequences given in AAA26281 to AAA26336 encode the
 CC human secreted proteins given in AAY91346 to AAY91449. The human secreted
 CC proteins can have activities based on the tissues and cells they are
 CC expressed in. Examples of the activities are: neuroprotective; neurotropic;

CC neuroleptic; antipsychotic; cerebroprotective; immunomodulatory;
 CC anti-microbial; cardanol; cytosolic; anti-inflammatory; haemostatic;
 CC anticonvulsant; and vasotonic. The polynucleotide and proteins may be
 CC used to prevent, treat or ameliorate a medical condition, e.g. by protein
 CC or gene therapy. Conditions treatable by the proteins of the invention
 CC include neural, reproductive, or immune disorders, especially
 CC immunodeficiency, infection, lymphomas, demyelinating diseases,
 CC auto-immunities, cancer, general microbial infection, inflammation,
 CC aneurysms and haemorrhages. Specific examples include: Alzheimer's
 CC disease; Parkinson's; Huntington's; Tourette syndrome; multiple
 CC sclerosis; meningitis; ischaemia; prostate cancer; mania; dementia;
 CC obsessive compulsive disorder and viral prophylaxis. The polynucleotides
 CC and proteins can also be used in the detection of disorders associated
 CC with the function of the protein, for example, the detection of
 CC developmental disorders, sexually-linked disorders, or disorders of the
 CC cardiovascular system. They may also be used as food additives or
 CC preservatives. AAA26272 to AAA26280 and AA91345 are sequences used in
 CC the exemplification of the present invention.

XX Sequence 123 AA:

Query Match 24.2%; Score 630; DB 21; Length 123;

Best Local Similarity 98.3%; Pred. No. 1e-42; Mismatches 2; Indels 0; Gaps 0;

Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 22 EHPADRACGACGACYSIHATMKRQAEEACILRGALSTVRACAEALRAVALLRAGP 81
 DB 1 EHPADRACGACGACYSIHATMKRQAEEACILRGALSTVRACAEALRAVALLRAGP 60

QY 82 GPGGSKDLFWALERRRSHCTLENEPRGFSWLSDDPGLESDPLQWVEPQRCTAR 141
 DB 61 GPGGSKDLFWALERRRSHCTLENEPRGFSWLSDDPGLESDPLQWVEPQRCTAR 120

QY 142 R 142
 DB 121 r 121

RESULT 13

AAE05343 AAE05343 standard; Protein; 492 AA.

AC AAE05343;

DT 12-SEP-2001 (first entry)

DE Mouse tumour endothelial marker I precursor protein.

XX mouse; cytosolic; anti-inflammatory; immunoregulatory; tissue integrity;

KM wound healing; immune response; vaccine; cancer; asthma; allergy;

KM cell trafficking; tumour endothelial marker I precursor protein;

OS Mus sp.

PM WO200148192-A1.

PD 05-JUL-2001.

PF 21-DEC-2000; 2000WO-NZ00256.

PR 23-DEC-1999; 99US-0171678.

PR 28-NOV-2000; 2000US-0724864.

PA (GENE-) GENESIS RES & DEV CORP LTD.

PI Watson JD, Morrison JG;

XX WPI; 2001-425665/45.
 DR N-PSDB; AAD10110.
 XX Novel isolated polypeptide useful to isolate corresponding interacting

PT proteins or other compounds, to quantitatively determine levels of
 PT interacting proteins or other compounds, and as therapeutic target
 XX Claim 6; Page 72-74; 101pp; English.

CC The patent discloses novel polynucleotides and their corresponding
 CC proteins which play a major role in induction of growth, cell migration
 CC and proliferation, cell-cell interaction and the differentiation of
 CC tissue-specific cells. These proteins are important in the maintenance
 CC of tissue integrity and thus are important in wound healing. They are
 CC useful in various assays to determine the biological activity, to raise
 CC antibodies, to isolate corresponding interacting proteins or other
 CC compounds, to quantitatively determine levels of interacting proteins or
 CC other compounds, and as therapeutic target in a whole range of disease
 CC states. Compositions comprising the novel proteins of the invention are
 CC useful for treating mammalian disorders. Polynucleotides of the invention
 CC are useful in genome and physical mapping, in positional cloning of
 CC genes, to tag or identify an organism or its reproductive material (as
 CC non-disruptive tags for marking organisms), and for the diagnosis and
 CC treatment of mammalian diseases which is the consequence of inappropriate
 CC expression of kinase genes. They are useful for promoting immune response
 CC as part of a vaccine or anti-cancer treatment, as target for cancer
 CC treatment, as immunoregulatory and anti-inflammatory molecule, as
 CC diagnostic for specific types of cancer and for development of an
 CC anti-cancer treatment, and as a target for antagonists in the treatment
 CC of diseases such as asthma and allergy. They are also useful to inhibit
 CC or enhance the activity of the soluble molecule that binds proteins of
 CC the invention, for tissue and neural regeneration, to promote or block
 CC cell trafficking, and as anti-inflammatory and/or vaccine adjuvant.
 CC The present sequence is mouse tumour endothelial marker I precursor
 CC protein.

XX Sequence 492 AA:

Query Match 12.9%; Score 336.5; DB 22; Length 492;

Best Local Similarity 32.8%; Pred. No. 1.9e-18; Mismatches 133; Indels 27; Gaps 12;

Matches 94; Conservative 33; Mismatches 133; Indels 27; Gaps 12;

QY 7 LCLLMQALMPGPGGHEPTADRACGACGACYSIHATMKRQAEEACILRGALSTVRA 66
 DB 3 LLawaavpalyqypwtpetpactags--scyalfrirttleawacrelggnlatpt 61

QY 67 GAELRAVALLLRAGGPGGSKDLFWALERRRSHCTLENEPRGFSWLSDDPGLESD 126
 DB 62 peeaqvdsilvgypang-----llwlgqrqarqg-pqrplrgifwtgq-----qd 109

QY 127 T--LQWVE-EPRQSTARRCAVLAQATGVEPRAGMKERHRLRNGVLCYQFVLCRA-- 181
 DB 110 tafnwaqpatpqpapqcaaleasg---ehrwlegstlavdgylcqfgeagacpajp 166

QY 182 PRGAASNLSTYRAPFOLHSAALDFSPGTEVSALCGQLPISVTCIADLEI-GARMDKLSG 240
 DB 167 levgagpavyltptflvssefawlpfgsvaavqagagysallckqsgygywsgtq- 225

QY 241 DVLCPGGRYLRAGKCAELPNCIDLI-GGPACCATGFELGKDGNSC 286
 DB 226 -plcpqtcgpdnggceh--ecveevdgavscrcsegfirlaadgfhsc 269

RESULT 14

AAW49879 AAW49879 standard; Protein; 652 AA.

AC AAW49879;

DT 26-OCT-1998 (first entry)

DE Amino acid sequence of human C1qR.

XX Human; C1q receptor protein; C1qR; phagocytosis; complement;

KM immune system; inflammation; prophylactic; genetic immune deficiency;
 KM HIV; cancer; chemotherapy; inhibition; vasculitis; sepsis; fragment;

Db	234	gshylckekapdvfdwgssgplcvcpkkygcfnmgngchqdcdfeegdgslfcgrprgfl	297
*Qy	239	SSDVLT-----CPCGRY-----LRAGKALP	260
Db	294	Iddltvcaarnpcssspcrgatclvgpnkgkntcrppqygldesqldevdecdqp	355
Qy	261	--NCLDLDGGFACECATGFE-----	278
Db	354	cagecvltpggfrccewvyepypgpbgacqvdecalgrpcagctnufhsccoe	413
Qy	279	--LGMDGNSC--VTSEEGP-----TLGTGTGPTRRPPAT	309
Db	414	gyvlagedtqcqdvdecvypgpgldscifntggsfhcgclpwglavmgvscmtmpvs	473
Qy	310	ATSPVPQRTWPIRVD-EKIGETPLVEEDNDSVTSIP-ELPRMGSSQSTMTLQSLQAES	366
Db	474	Lpppsp--pdcedkkegest-vp--raatasptirpegpkaptitrsplsda	555
Qy	367	KAT-----ITPSGS-----VICKNSTYSASAPAFDSSA-----VFET	401
Db	526	pitsaplknlapsgsvvrrepslhataasgpgpagdsstvatgnndgtcqklilly	585
Qy	402	FVSTAAVVILTMIVGLGVKLCEHESPSSQPKRESMPPELESDPEPPA	451
Db	586	ilgtvaillllal-algi-lvykkrrakreek-----ekkpgnaa	625
<hr/>			
RESULT	15		
AAV32345.	ID	AAV32345 standard; Protein: 652 AA.	
XX	XX	AAV32345;	
XX	XX	28-FEB-2000 (first entry)	
XX	DE	Human cell surface receptor C1qrp.	
C1qrp:	receptor; cell surface; transmembrane; glycoprotein; human; host defence; infection; HIV; immunodeficiency; therapy; immunostimulant; phagocytosis; signal transduction.		
OS	Homo sapiens.		
Key	Location/Qualifiers		
Peptide	1..21		
Protein	/note= "signal peptide"		
	22..652		
	/note= "mature protein"		
	22..580		
	/note= "extracellular domain"		
	581..605		
	/note= "transmembrane domain"		
	606..652		
	/note= "cytoplasmic domain"		
	260..301		
	/note= "epidermal growth factor-like domain 1"		
	302..344		
	/note= "epidermal growth factor-like domain 2"		
	345..384		
	/note= "epidermal growth factor-like domain 3"		
	385..426		
	/note= "epidermal growth factor-like domain 4"		
	427..468		
	/note= "epidermal growth factor-like domain 5"		
	325		
Misc-difference	644	/note= "N-glycosylated"	
	/note= "forms part of consensus motif recognised by tryptophan kinases"		
04-NOV-1999.	DD		

XX 29-APR-1999; 99WO-US09335.
 XX 30-APR-1998; 98US-0071386.
 XX (REGC) UNIV CALIFORNIA.
 XX Tenner AJ, Nepomuceno RR;
 XX WPI; 2000-062021/05.
 DR N-PSDB; AAZ34989.
 XX
 PT A new cell surface receptor protein used as a prophylactic for
 PT individuals at risk from infection, e.g. HIV.
 XX
 PS Claim 2; Fig 3; 49pp; English.

This sequence represents a novel human cell surface transmembrane glycoprotein receptor, designated C1qR, as deduced from cDNA (see AAZ34989) isolated from a 0937 library. C1qR has a predicted pI.wt. of 66,495 and a pI of 5.24. It plays a role in stimulating the classic complement component of the immune system, specifically in stimulating phagocytosis in cells without a concomitant increase in inflammation. Methods for detecting novel ligands for C1qR, including those which function as agonists or antagonists, are provided, as well as methods of determining compositions which effect the formation of an affinity complex between the C1qR and its ligand, and for determining compositions which modulate signal transduction via the C1qR. Transgenic animals can be created to aid in the study of the role of C1qR during growth and metabolism and as a model for disease states in which the normal level of C1qR is effected. The ability to regulate the phagocytic capacity of myeloid cells via the regulation of cell surface expression and function of C1qR will be valuable as a prophylactic treatment of individuals at risk from infection, particularly those with genetic immunodeficiencies, HIV infection, or undergoing cancer chemotherapy or high risk surgery.

Sequence 652 AA:

Query Match 11.8%; Score 307; DB 21; Length 652;
 Best Local Similarity 21.4%; Pred. No. 6.4e-16;
 Matches 139; Conservative 81; Mismatches 206; Indels 224; Gaps 28;

QY 1 MRPAFLCLLMQALMPGCGGEHPTADRAGCSAGACYSLHATMKQAEPACILRGGA 60
 DB 1 matsmgllllllltgpgagtgadteavvcvt-acytahsgklisaaeqnhcngngn 59
 QY 61 LSTRAGAE--LRVLA--LIRAGPGGGSKDILFWALERRSHCTLENEPLRGFSW 115
 DB 60 latvkskeaqhqvgrlaqlirreaaltarmsk---fwigldrekykclpdlplkgfsw 116
 QY 116 LSSDGLLESOTLQWVEPQRSTARRCA--VLQATGVEP--AGWKEMRC-----HL 164
 DB 117 Vg---ggedtqysnwkhelrnsclsrsvllldlsqpllnrlpkwsegpcspgspgs 173
 QY 165 RANGYLCKRYOFEVLCPAPRPGAAASNLRYRAPQLSHALDFSPGTEVSA----- 214
 DB 174 niegfvtckfsfkgmcrplalggpggvtyltqfqtssleavfasaanvacgegdket 233
 QY 215 -----LCRQQLP-----ISVTCIADETIGARWD-----KL 238
 DB 234 gshyflckekapdvfdwssgplcvspkygcnfnngschqdcfeggdgsflcgrpgffl 293
 QY 239 SGDVL-----CPGGRY-----LRAGKCAELP 260
 DB 294 lddlvtcasrncpssspcrgatcvl9phgknylcrp9yqldssqldcvdvdecdsp 353
 QY 261 ---NCIDLDLGGFACBACATGFE----- 278
 DB 354 caqecvnpmpgfrcecwgyrepgsgagcdvdecadlgrspcagqcnttdgsfnscsee 413

QY 279 ----LCKDRSC-----VTSGEOP-----TLGCTGYPTRRPPAT 309
 DB 414 gyvlagedgtqcdvdecvpgpplcdslcfnqtgsfhcgclpgwvllapngvscmtgpps 473
 QY 310 ATSPVQRTMPLRVD--EKLGEPPLVEQDNSVTSIP-ELPRMGSGSTSTLQMSLQAES 366
 DB 474 lpppsgp---pdeedkgekegst--vp---raatastptgpegtphatpstrpslsda 525
 QY 367 KAT-----ITPSGS-----VSKFNSTTSANPQAFDSSA-----VPEI 401
 DB 526 pltsaplklapsgsgvwrtpslnhataasgpgpeggdsavatqngdtdgklllly 585
 QY 402 FVSTAVVVLITMTYVLGLVKLCFHESSSQPKKESMGPPGLESDPEPPA 451
 DB 586 lltvvaillllal-alg1--lvyrkrakreekk-----ekpqnaa 625

Search completed: August 13, 2002, 09:33:29
 Job time: 129 sec

Tue Aug 13 09:56:25 2002

us-09-902-713b-96.rag

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OM protein - protein search, using sw model

Run on: August 13, 2002, 09:31:40 ; Search time 16.12 Seconds

(without alignments)
742.465 Million cell updates/sec

Title: US-09-902-713b-96

Perfect score: 2605

Sequence: 1 MRPAFALCLMQLMPPGPG.....LRDRAEGALLAESPLGSSDA 490

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/prodata/2/1aa/5A.COMB.pep.*
- 2: /cgn2_6/prodata/2/1aa/5B.COMB.pep.*
- 3: /cgn2_6/prodata/2/1aa/6A.COMB.pep.*
- 4: /cgn2_6/prodata/2/1aa/6B.COMB.pep.*
- 5: /cgn2_6/prodata/2/1aa/PCRTS.COMB.pep.*
- 6: /cgn2_6/prodata/2/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	11.8	652	2	US-08-751-305-2
2	230	8.8	572	6	5256770-7
3	227	8.7	446	1	US-08-307-444A-5
4	227	8.7	446	1	US-08-587-389-5
5	227	8.7	456	1	US-08-307-444A-3
6	227	8.7	456	1	US-08-307-444A-4
7	227	8.7	456	1	US-08-587-389-3
8	227	8.7	456	1	US-08-587-389-4
9	227	8.7	475	1	US-08-307-444A-1
10	227	8.7	475	1	US-08-307-444A-2
11	227	8.7	475	1	US-08-587-389-1
12	227	8.7	475	1	US-08-587-389-2
13	227	8.7	476	1	US-08-014-723-1
14	227	8.7	476	1	US-08-014-723-2
15	227	8.7	476	1	US-08-014-723-18
16	227	8.7	476	1	US-08-110-011A-1
17	227	8.7	476	1	US-08-110-011A-2
18	227	8.7	476	1	US-08-110-011A-18
19	227	8.7	494	1	US-08-014-723-14
20	227	8.7	494	1	US-08-014-723-16
21	227	8.7	494	1	US-08-110-011A-14
22	227	8.7	494	1	US-08-110-011A-16
23	227	8.7	497	1	US-08-312-870-3
24	227	8.7	498	2	US-08-733-564-2
25	227	8.7	575	1	US-08-261-206A-59
26	227	8.7	575	1	US-08-312-870-1
27	227	8.7	575	6	5466668-6

28	222	8.5	575	1	US-08-170-290A-54	Sequence 54, App1
29	175.5	6.7	215	1	US-08-312-870-5	Sequence 5, App11
30	133.5	5.1	443	2	US-08-833-963C-2	Sequence 2, App11
31	133.5	5.1	443	3	US-08-980-514-1	Sequence 1, App11
32	132.5	5.1	1065	2	US-08-400-159-8	Sequence 8, App11
33	132.5	5.1	1212	4	US-09-214-278-3	Sequence 3, App11
34	132.5	5.1	1238	4	US-09-214-278-5	Sequence 5, App11
35	132.5	5.1	1257	4	US-08-611-729A-8	Sequence 8, App11
36	130.5	5.0	985	5	PCT-US96-03916-6	Sequence 6, App11
37	130.5	5.0	985	5	PCT-US96-03916-66	Sequence 6, App11
38	126.5	4.9	1055	4	US-09-214-278-2	Sequence 2, App11
39	124	4.8	933	2	US-08-313-200-1	Sequence 1, App11
40	124	4.8	933	5	PCT-US93-03837-1	Sequence 1, App11
41	123	4.7	1148	4	US-08-882-046-4	Sequence 4, App11
42	122.5	4.7	1479	3	US-08-840-062-2	Sequence 2, App11
43	121.5	4.7	1455	3	US-08-840-062-5	Sequence 5, App11
44	118.5	4.5	1404	2	US-08-400-159-2	Sequence 2, App11
45	118.5	4.5	1404	3	US-08-611-729A-2	Sequence 2, App11

ALIGNMENTS

RESULT 1

US-08-751-305-2

Sequence 2, Application US/08751305

Patent No. 5965439

GENERAL INFORMATION:

APPLICANT: Tennet et al., Andrea J.

TITLE OF INVENTION: HOST DEFENSE ENHANCEMENT

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/751,305

FILING DATE: 18-NOV-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Wetherell, Jr., John R.

REGISTRATION NUMBER: 31,678

REFERENCE/DOCKET NUMBER: 07306/012001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 652 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-751-305-2

Query Match

Best Local Similarity 11.8%; Score 307; DB 2; Length 652;

Matches 139; Conservative 81; Mismatches 206; Indels 224; Gaps 28;

1 MRPAFALCLMQLMPPGPGGHPTRADACCSAGACTSLHATMKRQAAEEACILRGCA 60

1 MATSMGLILLILLILLITLPGAGTGADTEAVVCGT-ACVTAHSGKLSAEEAQNCHNONGN 59

61 LSTVVRAGAE---LRAVLA--LIRAGPDPGGGSKDLLEFVALERRRRSICTELEPLRFSW 115

Db 60 LATVSKKEAOHYORVLAOLLRREALTARMK - FWIGLOREKCKLDPSLPLGFSW 116
QY 116 LSSPGLESDTLQWVEEPORCTARCA - VQATGVPEP - AAWKEMK - HL 164
Db 117 VG - GGEIDP - GNMHKELENSCTISKRCVSLDLISQPLIPNLPKRWSEPCGSPGSPGS 173
QY 165 RANGVLCYOFELCPAPRGASNLSTYRPFOLHSAALDFSPGTEVSA - 214
Db 174 NIEGFVKESFKMCRPLALGGGYVLTPTPQTSSILENVPASAAVACGEDKDET 233
QY 215 -LCRGLP - ISVTCIDELGARD - KL 238
Db 234 QSHYFLCKEKAPVPYMGSSGGLCVSPKXGCMNNGCHODCEGDSFLGCGPGRFL 293
QY 239 SGDL - CPGRY - LAGACALP 260
Db 294 LDDLVCASRNPCSSPCGATVLCGPHKNTGRCPCGYDLDSDQDVYDCQDSP 353
QY 261 -NCDDIGFACCATGFE - 278
Db 354 CAOEVTNPGFRCRCWGWIEGCGEGACQDVDCALGRSPCAQCTINTDGFHSCDE 413
QY 279 -LKDGRSC - VTSGECP - TLGCTVPTRRPAT 309
Db 414 GVLAGEBGTQGDYDECYCPGRLCDSLCFTQSGFHGCLPGVVLAPNGVSTMGFVS 473
QY 310 ATSPVPORTWPIKVD - EKLGETPLVPBODNSVTIP - EIPMGSSOSTMTLOMSLOAES 366
Db 474 LGPPSGP - PDEEDKGEKST - VP - RAATSPTRGEGCPKAPTTSRSLSDA 525
QY 367 KAT - TSPGS - VISKRNSTISSATPOAFDSSA - VET 401
Db 526 PITSLPLMLAPSSSSGVRPSTHATAGPOEPAGDSSVATQNDGTGOKLILFY 585
QY 402 EVSTAVVVLITMTVLGLVLCHESSPSQPKRESMCPGLEDSPED 451
Db 586 ILGTVAALLLAL - ALGL - LVYRRKRAKEEK - EKKPQMA 625

RESULT 2
5256770-7
PATENT NO. 5256770
APPLICANT: GLASER, CHARLES B.; MORSE, MICHAEL J.; LIGHT, DAVID R.
TITLE OF INVENTION: OXIDATION RESISTANT THROMBOMODULIN ANALOGS
NUMBER OF SEQUENCES: 48
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/506,325
FILING DATE: 09-APR-1990
ID NO: 7
LENGTH: 572
5256770-7

Query Match 8.8%; Score 230; DB 6; Length 572;
Best Local Similarity 26.3%; Pred. No. 4.9e-11;
Matches 78; Conservative 38; Mismatches 119; Indels 62; Gaps 15;
QY 16 PGGGGEHPYADRAAGCSASACYSILHATMKROAEACILRGALSTVRAGAEIRAVLA 75
Db 23 PGGGSGCVDH - CFALYGPAPFLNASSQICDGLRLHMTVRSSVAADVISL 73
QY 76 LIRAGPGGSGKDLFWALE - RRSCHTLENEPLRGSWSSDPGLESPT 127
Db 74 LILN - GDGCVGRRL - WIGLQLPFGCGDPRKLG - PLRGQWVTGDNNTSYS - 119
QY 128 LQWVEEPORS - CTARCAVLOATGVPEPAGWKEMRCHLRANGVLCYKYOFEVLCP 180
Db 120 -RWARLDLNGAPLGLCVAVSAA - EATVPSEPI - WEBOCEYKADGLCEFHFPATCR 175
QY 181 -APRGAAS - NLSTYRAPFOLHSAALDFSPGTEVSALCGQLPISTCIADITGAW 235
Db 176 PLAVEGAAANAASITTYGPFARAGADFOALPVGSSAAV - APGLQIMCTAGNVQGHM 232

QY 236 DKLSDVLCPCGRY - LRAGKCALPNCDDLGAFACATGFEKGRSCVTS 289
Db 233 AR - EAPGAMDCSVENGCEHACNAIP - GAPRCQCPAGALQADGRSCTAS 280

RESULT 3
US-08-307-444A-5
Sequence 5, Application US/08307444A
Patent No. 5516659
GENERAL INFORMATION:
APPLICANT: NIT, ATSUSHI
APPLICANT: MORISHITA, HIDEAKI
APPLICANT: UEMURA, AKIO
APPLICANT: MOCHIDA, EI
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,444A
FILING DATE: 19-SEP-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/835,436
FILING DATE: 26-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: OLIFF, JAMES A.
REGISTRATION NUMBER: 27,075
REFERENCE/DOCKET NUMBER: JAO 27706.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
TELEX: 90-1799 PRO ALEX
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-307-444A-5

Query Match 8.7%; Score 227; DB 1; Length 446;
Best Local Similarity 25.7%; Pred. No. 6.2e-11;
Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;
QY 16 PGGGGEHPYADRAAGCSASACYSILHATMKROAEACILRGALSTVRAGAEIRAVLA 75
Db 5 PGGGSGCVDH - CFALYGPAPFLNASSQICDGLRLHMTVRSSVAADVISL 55
QY 76 LIRAGPGGSGKDLFWALE - RRSCHTLENEPLRGSWSSDPGLESPT 127
Db 56 LILN - GDGCVGRRL - WIGLQLPFGCGDPRKLG - PLRGQWVTGDNNTSYS - 102
QY 128 LQWVEEPORS - CTARCAVLOATGVPEPAGWKEMRCHLRANGVLCYKYOFEVLCP 180
Db 103 -RWARLDLNGAPLGLCVAVSAA - EATVPSEPI - WEBOCEYKADGLCEFHFPATCR 158
QY 181 -APRGAAS - NLSTYRAPFOLHSAALDFSPGTEVSALCGQLPISTCIADITGAW 229

Db 159 PLAVEGAAAAAIVTYGTFPARGADFOALPVGSSAAV---APLGIQLMCTAPPGAVOG 215
QY 230 -----EIGARD-----KLSGVLCP-GRYLRG---KCAEL--- 259
Db 216 HWAREAPGAMDCSVENGCGEHCACNAPGAPRCPPAGALQADGRSCGTASATOSCNDLCE 275
QY 260 ---PNCIDLDGGFACATGFEIGKDGRC 286
Db 276 HFCVPM-PDPPGSGSCMCEGYRLADQHRC 305

RESULT 4
US-08-587-389-5
; Sequence 5, Application US/08587389
; Patent No. 5695964
; GENERAL INFORMATION:

APPLICANT: NII, ATSUSHI
APPLICANT: MORISHITA, HIDEAKI
APPLICANT: UEMURA, AKIO
APPLICANT: MOCHIDA, EI
TITLE OF INVENTION: TRUNCATED THROMBOMODULIN, RECOMBINANT
TITLE OF INVENTION: PRODUCTION THEREOF, AND THERAPEUTIC AGENT (AS AMENDED)
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,389
FILING DATE: 17-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,444
FILING DATE: 19-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OLIF, JAMES A.
REGISTRATION NUMBER: 27,075
REFERENCE/DOCKET NUMBER: JAO 27706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
TELEX: 90-1799 PTO ALEX
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-587-389-5

Query Match 8.7%; Score 227; DB 1; Length 446;
Best Local Similarity 25.7%; Pred. No. 6,2e-11;
Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

QY 16 PGGGGEHPTADRGASGACYSLHATWKQAAEACTLRGALSTVRAGAEALRAVLA 75
Db 5 PPGGSGQCEVHD-----CFALYPGPATFLNASQICDGLGHMLTVRSSVAADVISL 55
QY 76 LIRAGGPPGGSGDLFWALE-----RRSHCTLENEPLRGSSWLSDDGGLSDPT 127

Db 56 LLN---GDGGVGRRL-WIGLQLPFGCGDPRKLG-----PLRGFWWTGDNNTSYS-- 102
QY 128 LOWVEEQR-----CTARCAVLQATGVPAGKEMKRECHLRANGYLCKTQFVLCF 180
Db 103 -RWARLDINAPLCGPLCAVNSAA--EATVPSERI-WEEQCEVKADGFLCEHPATCR 158
QY 181 -APRGAAS---NLSTRAPFQLHSAALDFSPPTGVSAICRGOLPISTYCIAD----- 229
Db 159 PLAVEGAAAAAIVTYGTFPARGADFOALPVGSSAAV---APLGIQLMCTAPPGAVOG 215
QY 230 -----EIGARD-----KLSGVLCP-GRYLRG---KCAEL--- 259
Db 216 HWAREAPGAMDCSVENGCGEHCACNAPGAPRCPPAGALQADGRSCGTASATOSCNDLCE 275
QY 260 ---PNCIDLDGGFACATGFEIGKDGRC 286
Db 276 HFCVPM-PDPPGSGSCMCEGYRLADQHRC 305

RESULT 5
US-08-307-444A-3
; Sequence 3, Application US/08307444A
; Patent No. 5516659
; GENERAL INFORMATION:

APPLICANT: NII, ATSUSHI
APPLICANT: MORISHITA, HIDEAKI
APPLICANT: UEMURA, AKIO
APPLICANT: MOCHIDA, EI
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,444A
FILING DATE: 19-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,436
FILING DATE: 26-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: OLIF, JAMES A.
REGISTRATION NUMBER: 27,075
REFERENCE/DOCKET NUMBER: JAO 27706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
TELEX: 90-1799 PTO ALEX
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-307-444A-3

Query Match 8.7%; Score 227; DB 1; Length 456;
Best Local Similarity 25.7%; Pred. No. 6,4e-11;
Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

QY 16 PGGGGEHPTADRGASGACYSLHATWKQAAEACTLRGALSTVRAGAEALRAVLA 75
Db 5 PPGGSGQCEVHD-----CFALYPGPATFLNASQICDGLGHMLTVRSSVAADVISL 55
QY 76 LIRAGGPPGGSGDLFWALE-----RRSHCTLENEPLRGSSWLSDDGGLSDPT 127

QY 16 PGGGGEHPADRRGCSAGACYSIHATMKROAEACILRGALSTVRAGELRAVLA 75
DB 5 POPGSGQCVHEHD-----CFALYGPATFTLNASQICDGLGHIMTVRSSVAADVLSL 55
QY 76 LLRAGPBGSGSKDLFWALE-----RRSHCTLENEPLRGFSWLSPPGGLSDPT 127
DB 56 LLN---GDGSGVGRRL-WIGLOLPBGCGDKPRKRG-----PLRGQVWTGNNNTSYS-- 102
QY 128 LOWEERFORS-----CTARRCAVLOATGVGPACMKRMCHLRANGTLCYQEVLCIP 180
DB 103 -RWARLDLNCAPLCPLCAVASNA--EATVPSEPI-WBEOQCEVAKADGFLCEHFPATCR 158
QY 181 --APRGAS--NLSTRAPFOLHSAALDFSPGTEVSALCRGOLPISTVCTAD----- 229
DB 159 PLAVEGMAAAVSTYGTGPFARAGADFOALPVGSSAAV---APLGLOMCTAPPGAVOG 215
QY 230 ---EIGARD-----KLSDVLCPCP-----GRLYAG---KCAEL-- 259
DB 216 HWAREAPGAMDCSVENGGEHACNAIPGAPRCQCPAGALADGRSCTASATQSCNDICE 275
DB 260 ---PNCIDLDGFACECATGFELGKDRSC 286
DB 276 HRCVBN-PDQPSYSQCMCTGYRLAADQRC 305

RESULT 6

US-08-307-444A-4

Sequence 4, Application US/08307444A

Patent No. 551659

GENERAL INFORMATION:

APPLICANT: NII, ATSUSHI

APPLICANT: MORISHITA, HIDEAKI

APPLICANT: UEMURA, AKIO

APPLICANT: MOCHIDA, EI

TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDES

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIFF & BERRIDGE

STREET: P.O. BOX 19928

CITY: ALEXANDRIA

STATE: VA

COUNTRY: USA

ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,444A

FILING DATE: 19-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/835,436

FILING DATE: 26-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: OLIFF, JAMES A.

REGISTRATION NUMBER: 27, 075

REFERENCE/DOCKET NUMBER: JAO 27706

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6400

TELEFAX: (703) 836-2787

TELEX: 90-1799 PTO ALEX

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 456 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYDROTHERICAL: NO

ANTI-SENSE: NO

US-08-307-444A-4

Query Match: 8.7%; Score 227; DB 1; Length 456;
Best Local Similarity: 25.7%; Pred. No. 6, 4e-11;
Matches: 85; Conservative: 36; Mismatches: 120; Indels: 90; Gaps: 18;

QY 16 PGGGGEHPADRRGCSAGACYSIHATMKROAEACILRGALSTVRAGELRAVLA 75
DB 5 POPGSGQCVHEHD-----CFALYGPATFTLNASQICDGLGHIMTVRSSVAADVLSL 55
QY 76 LLRAGPBGSGSKDLFWALE-----RRSHCTLENEPLRGFSWLSPPGGLSDPT 127
DB 56 LLN---GDGSGVGRRL-WIGLOLPBGCGDKPRKRG-----PLRGQVWTGNNNTSYS-- 102
QY 128 LOWEERFORS-----CTARRCAVLOATGVGPACMKRMCHLRANGTLCYQEVLCIP 180
DB 103 -RWARLDLNCAPLCPLCAVASNA--EATVPSEPI-WBEOQCEVAKADGFLCEHFPATCR 158
QY 181 --APRGAS--NLSTRAPFOLHSAALDFSPGTEVSALCRGOLPISTVCTAD----- 229
DB 159 PLAVEGMAAAVSTYGTGPFARAGADFOALPVGSSAAV---APLGLOMCTAPPGAVOG 215
QY 230 ---EIGARD-----KLSDVLCPCP-----GRLYAG---KCAEL-- 259
DB 216 HWAREAPGAMDCSVENGGEHACNAIPGAPRCQCPAGALADGRSCTASATQSCNDICE 275
DB 260 ---PNCIDLDGFACECATGFELGKDRSC 286
DB 276 HRCVBN-PDQPSYSQCMCTGYRLAADQRC 305

RESULT 7

US-08-587-389-3

Sequence 3, Application US/08587389

Patent No. 5695964

GENERAL INFORMATION:

APPLICANT: NII, ATSUSHI

APPLICANT: MORISHITA, HIDEAKI

APPLICANT: UEMURA, AKIO

APPLICANT: MOCHIDA, EI

TITLE OF INVENTION: TRUNCATED THROMBOMODULIN, RECOMBINANT

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIFF & BERRIDGE

STREET: P.O. BOX 19928

CITY: ALEXANDRIA

STATE: VA

COUNTRY: USA

ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/587,389

FILING DATE: 17-JAN-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/307,444

FILING DATE: 19-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: OLIFF, JAMES A.

REGISTRATION NUMBER: 27, 075

REFERENCE/DOCKET NUMBER: JAO 27706

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6400

TELEFAX: (703) 836-2787

TELEX: 90-1799 PTO ALEX

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 456 amino acids

US-08-587-389-3

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-587-389-3

Query Match 8.7% Score 227; DB 1; Length 456;
Best Local Similarity 25.7% Pred. No. 6.4e-11;
Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

QY 16 PGGGGEHPTADRACCSAGACYSLHHTMKROAAEACILRGALSTVRAGAELEAVLA 75
DB 5 PPGSGSQVEHD-----CFALYGPATFLNMQICDGLRGLMTVRSSVADVLSL 55
QY 76 LLRAGPGGGSKDLFWVALE-----RRSHCTLENEPLRGFSMLSPGGLSEPT 127
DB 56 LLN---GGGVGRRRL-WIGLDLPKCGDPRKLG-----PLRGFWVTGDNNTSYS-- 102
QY 128 LQWVEEPPORS-----CTARCAVLQATGVEPAGMKEMRCHLRANGYLCKYQFEVLCP 180
DB 103 -RMARLDLNGAPLCGLCVAVSA--EATVSEPT-WEEQCEVAKADGFLCEHFHPATCR 158
QY 181 -APRPGAS--NLSTAPFOLHSALDFSPGTEVSALCRGOLPIVTCIAD----- 229
DB 159 PLAVEPGAAVAASITGTGPFARAGADFOALPVGSSAAV--APLGLOIMCTAPPGAVOG 215
QY 230 -ELGARMD-----KLSDVLCPCP-----GRLVLAG--KKAEL-- 259
DB 216 HWAREAPGAMDCSVENGCEHACNAIPGAPRCQCPAGALQADGRSCTASATQSCNDLCE 275
QY 260 -PNCDDLDGFACECATGFEKDKGRSC 286
DB 276 HFCVPRN-PDQPGSYSCMCTGYRLAADQHRG 305

RESULT 8
US-08-587-389-4
Sequence 4, Application US/08587389
Patent No. 5695964
GENERAL INFORMATION:
APPLICANT: NII, ATSUSHI
APPLICANT: MORISHITA, HIDEAKI
APPLICANT: UEMURA, AKIO
APPLICANT: MOCHIDA, EI
TITLE OF INVENTION: TRUNCATED THROMBOMODULIN, RECOMBINANT
TITLE OF INVENTION: PRODUCTION THEREOF, AND THERAPEUTIC AGENT (AS AMENDED)
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIEFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,389
FILING DATE: 17-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,444
FILING DATE: 19-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OLIEFF, JAMES A.
REGISTRATION NUMBER: 27,075
REFERENCE/DOCKET NUMBER: JAO 27706

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
TELEX: 90-1799 PTO ALEX
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-587-389-4

Query Match 8.7% Score 227; DB 1; Length 456;
Best Local Similarity 25.7% Pred. No. 6.4e-11;
Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

QY 16 PGGGGEHPTADRACCSAGACYSLHHTMKROAAEACILRGALSTVRAGAELEAVLA 75
DB 5 PPGSGSQVEHD-----CFALYGPATFLNMQICDGLRGLMTVRSSVADVLSL 55
QY 76 LLRAGPGGGSKDLFWVALE-----RRSHCTLENEPLRGFSMLSPGGLSEPT 127
DB 56 LLN---GGGVGRRRL-WIGLDLPKCGDPRKLG-----PLRGFWVTGDNNTSYS-- 102
QY 128 LQWVEEPPORS-----CTARCAVLQATGVEPAGMKEMRCHLRANGYLCKYQFEVLCP 180
DB 103 -RMARLDLNGAPLCGLCVAVSA--EATVSEPT-WEEQCEVAKADGFLCEHFHPATCR 158
QY 181 -APRPGAS--NLSTAPFOLHSALDFSPGTEVSALCRGOLPIVTCIAD----- 229
DB 159 PLAVEPGAAVAASITGTGPFARAGADFOALPVGSSAAV--APLGLOIMCTAPPGAVOG 215
QY 230 -ELGARMD-----KLSDVLCPCP-----GRLVLAG--KKAEL-- 259
DB 216 HWAREAPGAMDCSVENGCEHACNAIPGAPRCQCPAGALQADGRSCTASATQSCNDLCE 275
QY 260 -PNCDDLDGFACECATGFEKDKGRSC 286
DB 276 HFCVPRN-PDQPGSYSCMCTGYRLAADQHRG 305

RESULT 9
US-08-307-444A-1
Sequence 1, Application US/08307444A
Patent No. 5516659
GENERAL INFORMATION:
APPLICANT: NII, ATSUSHI
APPLICANT: MORISHITA, HIDEAKI
APPLICANT: UEMURA, AKIO
APPLICANT: MOCHIDA, EI
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIEFF & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,444A
FILING DATE: 19-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/835,436
 FILING DATE: 26-FEB-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: OLIFF, JAMES A.
 REGISTRATION NUMBER: 27,075
 REFERENCE/DOCKET NUMBER: JAO 27706
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6400
 TELEFAX: (703) 836-2787
 TELEX: 90-1799 PTO ALEX
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 307-444A-1

Query Match 8.7%; Score 227; DB 1; Length 475;
 Best Local Similarity 25.7%; Pred. No. 6,7e-11;
 Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

QY 16 PGGGGEHPADRRAGCSAGCYSLHATMKRQAAEEACILRGALSTVRAGAELEAVLA 75
 DB 23 PPGGSGQVEHD-----CFALYGPATFLNLSQICGLHMTVRSVAADYISL 73
 QY 76 LRRGPGGSGSKDLFWALE-----RRSHCTLENEPLRGFSWLSDDPGLESST 127
 DB 74 LLN---GDGVGRRRL-WIGLQLEPPGCGDKPRKLG-----PLRGQWVTGDNNTSYS-- 120
 QY 128 LQWVEEPORS-----CTARRCAVLQATGVEPAGKEMKCHLRANGYLCKYQFEVLC 180
 DB 121 -RMARLDNGAPLPGPLCVAVSAA--EATVSEPI-WEEQCEVKADGFLCEHFPAITCR 176
 QY 181 --APRGAAS--NLSTAPRQULSAALDFSPPTETVSALCRGLPLSTVCTAD----- 229
 DB 177 PLAVEPAAAAAASITTYGTTPAARGADFOALPVGSSAAV---APLGLQIMCTAPPGAVOG 233
 QY 230 ---EIGARDW-----KLSGVDLCPCP-----GRYLIRAG--KCAEL-- 259
 DB 234 HWAREAPGAMDCSYENGCGEHCACNAIPGAPRCQCPAGALOADGRSCTASATQSCNDLCE 293
 QY 260 ---PNCIDLDGFGFACECATGFEELGKDGKRS 286
 DB 294 HFCVPM-PDOPGYSYSCMCEGYRLAADQHR 323

RESULT 10
 US-08-307-444A-2
 Sequence 2, Application US/08307444A
 Patent No. 531659

GENERAL INFORMATION:
 APPLICANT: NII, ATSUSHI
 APPLICANT: MORISHITA, HIDEAKI
 APPLICANT: UEMURA, AKIO
 APPLICANT: MOCHIDA, EI
 TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDES
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OLIFF & BERRIDGE
 STREET: P.O. BOX 19928
 CITY: ALEXANDRIA
 STATE: VA
 COUNTRY: USA
 ZIP: 22320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/307,444A
 FILING DATE: 19-SEP-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/835,436
 FILING DATE: 26-FEB-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: OLIFF, JAMES A.
 REGISTRATION NUMBER: 27,075
 REFERENCE/DOCKET NUMBER: JAO 27706
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6400
 TELEFAX: (703) 836-2787
 TELEX: 90-1799 PTO ALEX
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 US-08-307-444A-2

Query Match 8.7%; Score 227; DB 1; Length 475;
 Best Local Similarity 25.7%; Pred. No. 6,7e-11;
 Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

QY 16 PGGGGEHPADRRAGCSAGCYSLHATMKRQAAEEACILRGALSTVRAGAELEAVLA 75
 DB 23 PPGGSGQVEHD-----CFALYGPATFLNLSQICGLHMTVRSVAADYISL 73
 QY 76 LRRGPGGSGSKDLFWALE-----RRSHCTLENEPLRGFSWLSDDPGLESST 127
 DB 74 LLN---GDGVGRRRL-WIGLQLEPPGCGDKPRKLG-----PLRGQWVTGDNNTSYS-- 120
 QY 128 LQWVEEPORS-----CTARRCAVLQATGVEPAGKEMKCHLRANGYLCKYQFEVLC 180
 DB 121 -RMARLDNGAPLPGPLCVAVSAA--EATVSEPI-WEEQCEVKADGFLCEHFPAITCR 176
 QY 181 --APRGAAS--NLSTAPRQULSAALDFSPPTETVSALCRGLPLSTVCTAD----- 229
 DB 177 PLAVEPAAAAAASITTYGTTPAARGADFOALPVGSSAAV---APLGLQIMCTAPPGAVOG 233
 QY 230 ---EIGARDW-----KLSGVDLCPCP-----GRYLIRAG--KCAEL-- 259
 DB 234 HWAREAPGAMDCSYENGCGEHCACNAIPGAPRCQCPAGALOADGRSCTASATQSCNDLCE 293
 QY 260 ---PNCIDLDGFGFACECATGFEELGKDGKRS 286
 DB 294 HFCVPM-PDOPGYSYSCMCEGYRLAADQHR 323

RESULT 11
 US-08-587-389-1
 Sequence 1, Application US/08587389
 Patent No. 569564

GENERAL INFORMATION:
 APPLICANT: NII, ATSUSHI
 APPLICANT: MORISHITA, HIDEAKI
 APPLICANT: UEMURA, AKIO
 APPLICANT: MOCHIDA, EI
 TITLE OF INVENTION: TRUNCATED THROMBOMODULIN, RECOMBINANT
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OLIFF & BERRIDGE
 STREET: P.O. BOX 19928
 CITY: ALEXANDRIA

STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,389
FILING DATE: 17-JAN-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/307,444
FILING DATE: 19-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OLIFE, JAMES A.
REGISTRATION NUMBER: 27,075
REFERENCE/DOCKET NUMBER: JAO 27706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
TELEX: 90-1799 PTO ALEX
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-587-389-1

Query Match 8.7%; Score 227; DB 1; Length 475;
Best Local Similarity 25.7%; Pred. No. 6.7e-11;
Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

QY 16 PPGGGEHPTADRAGSAGACYSLSHATMKRQAEACILRGALSTVRAGAEIARAVLA 75
DB 23 PPGGSGQCVCHD-----CFALYPGPATFLMASQICDGLRGLMTVRSVAADVISL 73
QY 76 LIRAGPFGGSGKDLLEWVALE-----RRSHCTLENEPLRGFSWLSDPGGLESPT 127
DB 74 LLN---GDGCVGRRRL-WIGLQLPCCGDKPKRLG-----PLRGQWVTGNNNTSYS-- 120
QY 128 LQWVEEPORS-----CTARRCAVLAQTGVEYPAGWKMKRCHLRANGYLCKYQFEVLCP 180
DB 121 -RWARLDLNGADPLCGPLCAVSA--EATVPSEPI-WEDQCEVKAADGFLCEHFEPATCR 176
QY 181 -APRGAS--NLSYRPFQLSALDFSPGTEVSALCGQLPISTVCIAD----- 229
DB 177 PLAVEPQAANAIVSTYGGPFAARGADPQALPVGSSAAV---APLGLQMLCTAPPGAVOG 233
QY 230 ----EIGARM-----KLSGDVLCPCP-----GRYLARG--KCAEL-- 259
DB 234 HMARAPGAMDCSVENGGEHACNAIPGAPRCQCPAGALQADGRCTASATOSCNLDCE 293
QY 260 ----PNCIDDLGFGACECATGFEIGKDRSC 286
DB 294 HFCVFN-PDQPGSYSCMCTGYRLAADQHRG 323

RESULT 12
US-08-587-389-2
Sequence 2, Application US/08587389
Patent No. 5693964
GENERAL INFORMATION:
APPLICANT: NII, ATSUSHI
APPLICANT: MORISHITA, HIDEAKI
APPLICANT: UEMURA, AKIO
APPLICANT: MOCHIDA, ET

TITLE OF INVENTION: TRUNCATED THROMBOMODULIN, RECOMBINANT
TITLE OF INVENTION: PRODUCTION THEREOF, AND THERAPEUTIC AGENT (AS AMENDED)
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFE & BERRIDGE
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,389
FILING DATE: 17-JAN-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/307,444
FILING DATE: 19-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OLIFE, JAMES A.
REGISTRATION NUMBER: 27,075
REFERENCE/DOCKET NUMBER: JAO 27706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
TELEX: 90-1799 PTO ALEX
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-587-389-2

Query Match 8.7%; Score 227; DB 1; Length 475;
Best Local Similarity 25.7%; Pred. No. 6.7e-11;
Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

QY 16 PPGGGEHPTADRAGSAGACYSLSHATMKRQAEACILRGALSTVRAGAEIARAVLA 75
DB 23 PPGGSGQCVCHD-----CFALYPGPATFLMASQICDGLRGLMTVRSVAADVISL 73
QY 76 LIRAGPFGGSGKDLLEWVALE-----RRSHCTLENEPLRGFSWLSDPGGLESPT 127
DB 74 LLN---GDGCVGRRRL-WIGLQLPCCGDKPKRLG-----PLRGQWVTGNNNTSYS-- 120
QY 128 LQWVEEPORS-----CTARRCAVLAQTGVEYPAGWKMKRCHLRANGYLCKYQFEVLCP 180
DB 121 -RWARLDLNGADPLCGPLCAVSA--EATVPSEPI-WEDQCEVKAADGFLCEHFEPATCR 176
QY 181 -APRGAS--NLSYRPFQLSALDFSPGTEVSALCGQLPISTVCIAD----- 229
DB 177 PLAVEPQAANAIVSTYGGPFAARGADPQALPVGSSAAV---APLGLQMLCTAPPGAVOG 233
QY 230 ----EIGARM-----KLSGDVLCPCP-----GRYLARG--KCAEL-- 259
DB 234 HMARAPGAMDCSVENGGEHACNAIPGAPRCQCPAGALQADGRCTASATOSCNLDCE 293
QY 260 ----PNCIDDLGFGACECATGFEIGKDRSC 286
DB 294 HFCVFN-PDQPGSYSCMCTGYRLAADQHRG 323

RESULT 13
US-08-014-723-1

Sequence 1, Application US/08014723
Patent No. 5273962

GENERAL INFORMATION:

APPLICANT: Doi, Takeshi
APPLICANT: Iwasaki, Akio
APPLICANT: Saino, Yushi
APPLICANT: Kimura, Shigeru
APPLICANT: Okuchi, Masao
TITLE OF INVENTION: Thrombin-Binding Substance and Process
TITLE OF INVENTION: For Preparing the Same
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,723
FILING DATE: 19930208
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5273962man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-071-0 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-014-723-1

Query Match 8.7% Score 227; DB 1; Length 476;
Best Local Similarity 25.7%; Pred. No. 6.8e-11;

Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

16 PGGGGEHPTADRGASGACYSILHATMRQAEEACILRGALSTVRAGAEIRAVLA 75
5 PGGGSGQCVEND-----CFALYGPATFLNASQIDGLRGLMTVRSSAADVISL 55
DB 76 ILRAGPGGGSKDLLFWALE-----RRSHCTLENEPLRGFSWSSDPGLESDT 127
56 LLN---GGGAGVGRRL-WIGIDLPCCGDPKRLG-----PLRGFOWTGDNNITSYS-- 102
QY 128 LOWEPEPORS-----CTARCAVLOATGVEPAGMKEMKCHLRANGYLCKYQEVLC 180
DB 103 -RMARLDLNGAPLCPICVAVSA--EATVSEPT-WEBOQCEVKADGFLCEHFPATCR 158
QY 181 -APRGAAS--NLSTAPFOLHSALDPSPTGEVSALCRGOLPISTVICIAD----- 229
DB 159 PLAVEPGAAAIAVSIYTGPFPAARGADFOALPVSSAAV--APLIGQLMCTAPPGAVOG 215
QY 230 -----ETGARMD-----KLSGDVLCPCP-----GRYLARG--KCAEL-- 259
DB 216 HWAIEAPGAMDCSVENGGEHACNAIPGAPRCQCPAGALADGRSCTASATQSCNDICE 275
QY 260 -----PNCIDLDGFAECATGFEIGKDGRC 286
DB 276 HFCVNP-PDQPGSYSCMCTGYRLAADQHRG 305

RESULT 14
US-08-014-723-2

Sequence 2, Application US/08014723
Patent No. 5273962

GENERAL INFORMATION:

APPLICANT: Doi, Takeshi
APPLICANT: Iwasaki, Akio
APPLICANT: Saino, Yushi
APPLICANT: Kimura, Shigeru
APPLICANT: Okuchi, Masao
TITLE OF INVENTION: Thrombin-Binding Substance and Process
TITLE OF INVENTION: For Preparing the Same
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,723
FILING DATE: 19930208
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5273962man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-071-0 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-014-723-2

Query Match 8.7% Score 227; DB 1; Length 476;
Best Local Similarity 25.7%; Pred. No. 6.8e-11;

Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

16 PGGGGEHPTADRGASGACYSILHATMRQAEEACILRGALSTVRAGAEIRAVLA 75
5 PGGGSGQCVEND-----CFALYGPATFLNASQIDGLRGLMTVRSSAADVISL 55
DB 76 ILRAGPGGGSKDLLFWALE-----RRSHCTLENEPLRGFSWSSDPGLESDT 127
56 LLN---GGGAGVGRRL-WIGIDLPCCGDPKRLG-----PLRGFOWTGDNNITSYS-- 102
QY 128 LOWEPEPORS-----CTARCAVLOATGVEPAGMKEMKCHLRANGYLCKYQEVLC 180
DB 103 -RMARLDLNGAPLCPICVAVSA--EATVSEPT-WEBOQCEVKADGFLCEHFPATCR 158
QY 181 -APRGAAS--NLSTAPFOLHSALDPSPTGEVSALCRGOLPISTVICIAD----- 229
DB 159 PLAVEPGAAAIAVSIYTGPFPAARGADFOALPVSSAAV--APLIGQLMCTAPPGAVOG 215
QY 230 -----ETGARMD-----KLSGDVLCPCP-----GRYLARG--KCAEL-- 259
DB 216 HWAIEAPGAMDCSVENGGEHACNAIPGAPRCQCPAGALADGRSCTASATQSCNDICE 275
QY 260 -----PNCIDLDGFAECATGFEIGKDGRC 286
DB 276 HFCVNP-PDQPGSYSCMCTGYRLAADQHRG 305

Tue Aug 13 09:56:27 2002

us-09-902-713b-96.ra1

Biochem. J. 295, 131-140, 1993
 A>Title: Identification of the predominant glycosaminoglycan attachment site in soluble
 A:Reference number: S38954; MUID:94029900
 A:Accession: S38954
 A:Molecule type: protein
 A:Residues: 475-491, 'X', 493-494 <GER>
 A>Note: The residue designated 'X' was determined to be a Ser with covalently bound chor
 R:Meininger, D.P.; Komives, E.A.
 Submitted to the Brookhaven Protein Data Bank, September 1995
 A:Reference number: A67369; PDB:1ZAG
 A:Contents: annotation: conformation and disulfide bond assignments by (1)H-NMR, residue
 R:Tulinsky, A.; Mathews, I.I.
 Submitted to the Brookhaven Protein Data Bank, August 1994
 A:Reference number: A52804; PDB:1HLT
 A:Contents: annotation: X-ray crystallography, 3.0 angstroms, residues 426-442
 R:Hirabai, R.; Komives, E.A.; Ni, F.
 Submitted to the Brookhaven Protein Data Bank, November 1995
 A:Reference number: A65583; PDB:1FGD
 A:Contents: annotation: conformation by (1)H-NMR, residues 427-444
 R:abdal, R.; Komives, E.A.; Ni, F.
 Protein Sci. 5, 195-203, 1996
 A>Title: Structural resiliency of an EGF-like subdomain bound to its target protein, the
 A:Reference number: A58595; MUID:96276211
 A:Contents: annotation: conformation by (1)H-NMR
 C:Genetics:
 A:Gene: GDB:THED
 A:Cross-references: GDB:119613; OMIM:188040
 A:Map position: 20p11.2-20p11.2
 A:Introns: #status absent
 C:Complex: homodimer, urinary form
 C:Function:
 A:Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activat
 A:Pathway: blood coagulation moderation
 A>Note: the membrane-bound form is located on the endothelium luminal surface of arterie
 A:Note: Chromomodulin complexed with the membrane-bound form is subject to endocytosis
 C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology
 C:Keywords: anticoagulant; beta-hydroxyaspartate; beta-hydroxyaspartic acid; blood coag
 e protein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-575/Product: thrombomodulin, membrane-bound form #status predicted <MAT>
 F:19-513/Domain: extracellular #status predicted <EXT>
 F:19-486/Product: thrombomodulin, urinary form #status experimental <MAU>
 F:24-167/Domain: C-type lectin homology <LCH>
 F:177-199/Region: PEST sequence
 F:201-233/Region: PEST sequence
 F:245-280/Domain: EGF homology <EG1>
 F:288-323/Domain: EGF homology <EG2>
 F:362-362/Domain: EGF homology <EG3>
 F:404-404/Domain: EGF homology <EG4>
 F:408-439/Domain: EGF homology <EG5>
 F:445-480/Domain: EGF homology <EG6>
 F:485-513/Region: PEST sequence
 F:517-539/Domain: transmembrane #status predicted <TMN>
 F:540-575/Domain: intracellular #status predicted <INT>
 F:47,115,116,382,409/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:174,225,411,504/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F:245-256,252-265,292-308,310-323,329-340,336-349,351-362,369-378,374-38
 F:334,498/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:342/Modified site: erythro-beta-hydroxyaspartate (Asn) #status experimental
 F:490,492/Binding site: chromotrolin sulfate (Ser) (covalent) (partial) #status experim

Query Match 8.7%; Score 227; DB 1; Length 575;
 Best Local Similarity 25.7%; Pred. No. 2.2e-06;
 Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

OY 16 PEPGGGEHTARACCSAGACTYSHHATMKRQAEEACILRGALSTVRAGAEELRAVIA 75
 DB 23 PEPGGSGQCEVHD-----CFALYGPATPELNSQCDCGLRGLIMTVRSVAADVISL 73
 OY 76 LTRAPGCGGSGKDLFWVALE-----RRRSCHLENPPLNGFSWLSDDPGGLESST 127

Db 74 LTN--GDGGVGRRL--WIGLPLPGCGDPPKRLG-----PLRGFWYTGDNNTSYS-- 120
 OY 128 LOWVEEPPRS-----CTARCAVLATGTVGEVAGKEKRECHIRANGYLCKQFVEYLC 180
 Db 121 -RMARLDNGAFILCGPLCAVAASA--EATVPSEPT--WEEOCEVKADGFCIEHFPAATCH 176
 OY 181 --ADPGGAAS--NLSYRAPFOLHSALDFSPGTEVSALCRQDLPSTVYCTIAD----- 229
 Db 177 PLAVEPGAAAAVAASITGTPEFAANGADFOALPVGSSAAV--APLGIQLMCTAPPAAVGG 233
 OY 230 ----ELIARD-----KLSGVLCPCP-----GRLRAG--KCAEL-- 259
 Db 234 HMAEAPGADMCVENGCGEHCACNAIFGAPRCOCPPAGALOADGRCTASATQSCNDLCE 293
 OY 260 ----PNCIDLDLGRACATGFEIKGRGRC 286
 Db 294 HFCVFN-PDGPVSYSCEHGYTLADQHRC 323

RESULT 2
 A60501
 thrombomodulin precursor - mouse
 N:Alternate names: fetomodulin
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
 C:Accession: S08488; A52001; A60501
 R:Dittman, W.A.; Majerus, P.W.
 Nucleic Acids Res. 17, 802, 1989
 A>Title: Sequence of a cDNA for mouse thrombomodulin and comparison of the predicted
 A:Reference number: S08488; MUID:89128454
 A:Accession: S08488
 A:Molecule type: mRNA
 A:Residues: 1-577 <DIT>
 A:Cross-references: EMBL:X14432; NID:954781; PID:CAA32597.1; PID:954782
 R:Dittman, W.A.; Kumada, T.; Sadler, J.E.; Majerus, P.W.
 J. Biol. Chem. 263, 15815-15822, 1988
 A>Title: The structure and function of mouse thrombomodulin. Phorbol myristate acetat
 A:Reference number: A12001; MUID:89008498
 A:Accession: A12001
 A:Molecule type: mRNA
 A:Residues: 97-577 <D12>
 A:Cross-references: GB:J04060
 R:Imada, S.; Yamaguchi, H.; Nagumo, M.; Katayanagi, S.; Iwasaki, H.; Imada, M.
 Dev. Biol. 140, 113-122, 1990
 A>Title: Identification of fetomodulin, a surface marker protein of fetal development
 A:Reference number: A60501; MUID:90292331
 A:Accession: A60501
 A:Molecule type: protein
 A:Residues: 19-22;330-343;479-489;545-555;562-575 <IMA>
 C:Comment: Thrombomodulin binds to and internalizes with thrombin. It is also a cofac
 C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology
 C:Keywords: anticoagulant; membrane protein; phosphoprotein; receptor
 F:24-165/Domain: C-type lectin homology <LCH>
 F:244-279/Domain: EGF homology <EG1>
 F:287-322/Domain: EGF homology <EG2>
 F:328-361/Domain: EGF homology <EG3>
 F:368-403/Domain: EGF homology <EG4>
 F:407-438/Domain: EGF homology <EG5>
 F:444-479/Domain: EGF homology <EG6>

Query Match 7.4%; Score 192; DB 2; Length 577;
 Best Local Similarity 24.7%; Pred. No. 6.4e-06;
 Matches 75; Conservative 34; Mismatches 125; Indels 70; Gaps 15;

OY 37 CYSIHHATMKRQAEEACILRGALSTVRAGAEELRAVIALLRAGPGGSGKDLFWVAL 96
 Db 35 CFALDPGAPATPELDASQCRLOGLHMTVRSVAADVISL-----SQSSMDLGPWIGL 88
 OY 97 ERRRSHC--TLENPELRGFSWLSDDPGLESPTLQWVEEPPQSCARRAVLQATGAV-- 152
 Db 89 QLPQG--CDPVEHLGPIRGITQWYTGDN--HTISRWARPNDQ--TAPLGLPCLVTVSTAT 142

GenCore version 4.5.
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OM protein - protein search, using sw model

Run on: August 13, 2002, 09:33:30 ; Search time 13.46 Seconds

(without alignments)
1409.553 Million cell updates/sec

Title: US-09-902-713b-96

Perfect score: 2605

Sequence: 1 MRPAFALCLLMQALMPGPG.....LRDRAEGALLAESPLGSSDA 490

ALIGNMENTS

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

1 number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	8.7	575	1 TRBM_HUMAN	P07204 homo sapien
2	192	7.4	577	1 TRBM_MOUSE	P15306 mus musculu
3	143.5	5.5	273	1 MT75_MOUSE	Q9bhp2 homo sapien
4	139.5	5.4	273	1 MT75_MOUSE	Q9cxm0 mus musculu
5	134.5	5.2	443	1 FB14_CRIGR	O53058 cricetulus
6	133.5	5.1	443	1 FB14_HUMAN	O95967 homo sapien
7	130.5	5.0	443	1 FB14_MOUSE	O9wvj9 mus musculu
8	128	4.9	592	1 DLT3_MOUSE	O88516 mus musculu
9	126	4.8	589	1 DLT3_RAT	O88671 rattus norv
10	126	4.8	3695	1 LMA5_HUMAN	O15330 homo sapien
11	124.5	4.8	2477	1 F1NC_RAT	P04937 rattus norv
12	124	4.7	933	1 PERT_HUMAN	P07202 homo sapien
13	122	4.7	618	1 DLT3_HUMAN	O9nyj7 homo sapien
14	119	4.6	646	1 LEM3_BOVIN	P42201 bos taurus
15	119	4.6	2871	1 FBNI_PIG	O9lt36 sus scrofa
16	119	4.6	2907	1 FBNI_MOUSE	O61555 mus musculu
17	118.5	4.5	1408	1 SERR_DROME	P18168 drosophila
18	118.5	4.5	4655	1 LRP2_HUMAN	P98164 homo sapien
19	118	4.5	448	1 FBLS_HUMAN	O9uwx5 homo sapien
20	117.5	4.5	448	1 FBLS_MOUSE	O9wvh9 mus musculu
21	117.5	4.5	2318	1 NTC3_MOUSE	O61882 mus musculu
22	117	4.5	2871	1 FBNI_BOVIN	P98133 bos taurus
23	117	4.5	2871	1 FBNI_HUMAN	O61554 mus musculu
24	117	4.5	2871	1 FBNI_MOUSE	O61554 mus musculu
25	116.5	4.5	448	1 FBLS_RAT	O9wvh9 rattus norv
26	116	4.5	2911	1 FBNI_MOUSE	P35556 homo sapien
27	115	4.4	174	1 PAR3_HUMAN	O09949 mus musculu
28	115	4.4	176	1 SCAP_CRIGR	P97260 cricetulus
29	115	4.4	4753	1 LRP_CAEEL	Q04833 caenorhabdi
30	114.5	4.4	1456	1 MANR_HUMAN	P22897 homo sapien
31	114.5	4.4	1964	1 NTC4_MOUSE	P31695 mus musculu
32	113.5	4.4	676	1 PRPS_HUMAN	P07225 homo sapien
33	113.5	4.4	2254	1 CCAG_RAT	O54898 rattus norv

RESULT	ID	TRBM_HUMAN	STANDARD	PRT	575 AA
34	113	4.3	2139	1 CRB_DROME	P10040 drosophila
35	112.5	4.3	909	1 LDLI_XENLA	O99087 xenopus lae
36	112.5	4.3	4660	1 LRP2_RAT	P98158 rattus norv
37	112	4.3	1221	1 FB12_MOUSE	P37889 mus musculu
38	111	4.3	596	1 MKC7_YEAST	P53379 saccharomyc
39	111	4.3	2437	1 NOTC_BRARE	P46530 brachydanio
40	110.5	4.2	1375	1 NID2_HUMAN	Q14112 homo sapien
41	110	4.2	675	1 PRTS_MOUSE	O08761 mus musculu
42	110	4.2	776	1 SNIL_RAT	O9rlu5 rattus norv
43	109.5	4.2	649	1 PRTS_MACMU	O28520 macaca mula
44	109.5	4.2	926	1 PRTS_PIG	P09933 sus scrofa
45	109	4.2	675	1 PRTS_RAT	P53813 rattus norv

RESULT 1
ID TRBM_HUMAN
AC P07204;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Thrombomodulin precursor (Fetomodulin) (TM) (CD141 antigen).
GN THBD OR THRM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88004395; PubMed=2820710;
RA Suzuki K., Kusumoto H., Devashiki Y., Nishioka J., Maruyama I., Zushi M., Kawahara S., Honda G., Yamamoto S., Horiguchi S.;
RT "Structure and expression of human thrombomodulin, a thrombin receptor on endothelium acting as a cofactor for protein C activation."
RT EMBO J. 6:1891-1897(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88024950; PubMed=2822087;
RA Men D., Dittman W.A., Ye R.D., Deaven L.L., Majerus P.W., Sadler J.E.;
RT "Human thrombomodulin: complete cDNA sequence and chromosome localization of the gene."
RT Biochemistry 26:4350-4357(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87317655; PubMed=2819876;
RA Jackson R.W., Beeler D.L., Fritz L., Soff G., Rosenberg R.D.;
RT "Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDNA and gene predict protein structure and suggest sites of regulatory control."
RT Proc. Natl. Acad. Sci. U.S.A. 84:6425-6429(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227901; PubMed=2836377;
RA Shirai T., Shiojiri S., Ito H., Yamamoto S., Kusumoto H., Devashiki Y., Maruyama I., Suzuki K.;
RT "Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed activation of protein C."
RT J. Biochem. 103:281-285(1988).
RN [5]
RP SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beare D.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R., Coulson A.G., Coville G.J., Deadman R., Dhami P., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Graftman D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivasalho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McEay K., Murray A.A.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Philimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.E., Williams S.A.,
RA Wilmshurst L., Wray P.W., Hubbard T., Duden R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RA "The DNA sequence and comparative analysis of human chromosome 20.",
RA Nature 414:865-871(2001).
RA [6]
RA CARBOHYDRATE-LINKAGE SITE SER-492, AND MUTAGENESIS:
RA MEDLINE=94029900; PubMed=8216207;
RA Grinnell B.W., Hassell T., Vlahos C.J., Parkinson J.F., Bang N.U.,
RA "Identification of the predominant glycosaminoglycan-attachment site
RA in soluble recombinant human thrombomodulin: potential regulation of
RA functionality by glycosyltransferase competition for serine74.",
RA Biochem. J. 295:131-140(1993).
RA [7]
RA STRUCTURE BY NMR OF 389-407
RA MEDLINE=96007474; PubMed=7559494;
RA Adler M., Seto M.H., Nitecki D.E., Lin J.H., Light D.R., Morser J.,
RA "The structure of a 19-residue fragment from the C-loop of the fourth
RA epidermal growth factor-like domain of thrombomodulin.",
RA J. Biol. Chem. 270:23366-23372(1995).
RA [8]
RA STRUCTURE BY NMR OF 364-407
RA MEDLINE=96100636; PubMed=8528067;
RA Meuninger D.P., Hunter M.J., Komives E.A.,
RA "Synthesis, activity, and preliminary structure of the fourth
RA EGF-like domain of thrombomodulin.",
RA Protein Sci. 4:1683-1695(1995).
RA [9]
RA STRUCTURE BY NMR OF 427-444
RA MEDLINE=95034791; PubMed=7947766;
RA Sriivasan J., Hu S., Hrabal R., Zhu Y., Komives E.A., Ni F.,
RA "Thrombin-bound structure of an EGF subdomain from human
RA thrombomodulin determined by transferred nuclear Overhauser
RA effects.",
RA Biochemistry 33:13553-13560(1994).
RA [10]
RA STRUCTURE BY NMR OF 427-444
RA MEDLINE=96276211; PubMed=8745396;
RA Hrabal R., Komives E.A., Ni F.,
RA "Structural resiliency of an EGF-like subdomain bound to its target
RA protein, thrombin.",
RA Protein Sci. 5:195-203(1996).
RA [11]
RA STRUCTURE BY NMR OF 405-444
RA MEDLINE=98035729; PubMed=9367781;
RA Sampoli Benitez B.A., Hunter M.J., Meuninger D.P., Komives E.A.,
RA "Structure of the fifth EGF-like domain of thrombomodulin: an
RA EGF-like domain with a novel disulfide-bonding pattern.",
RA J. Mol. Biol. 273:913-926(1997).
RA [12]
RA VARIANT TED TYR-486:
RA MEDLINE=95111115; PubMed=7811989;
RA Oehlin A.-K., Marlar R.A.,
RA "The first mutation identified in the thrombomodulin gene in a
RA 45-year-old man presenting with thromboembolic disease.",
RA Blood 85:330-336(1995).
RA [13]
RA VARIANT TED Y-486, AND VARIANTS T-43; A-79; S-495 AND L-501.
RA MEDLINE=97341986; PubMed=9198166;
RA Oehlin A.-K., Norlund L., Marlar R.A.,
RA "Thrombomodulin gene variations and thromboembolic disease.",
RA Thromb. Haemost. 78:396-400(1997).
RA [14]
RA VARIANT VAL-473:
RA MEDLINE=97206518; PubMed=9157575;
RA Norlund L., Holm J., Zoller B., Oehlin A.-K.,
RA "A common thrombomodulin amino acid dimorphism is associated with
RA myocardial infarction.",
RA Thromb. Haemost. 77:248-251(1997).
RA [15]
RA VARIANT THR-43:
RA MEDLINE=99057299; PubMed=9843165;
RA Doggen C.J.M., Kunz G., Rosendaal F.R., Lane D.A., Vos H.L.,
RA Strubbs P.J., Manger Cats V., Ireland H.,
RA "A mutation in the thrombomodulin gene, 127G to A coding for Ala25Thr,
RA and the risk of myocardial infarction in men.",
RA Thromb. Haemost. 80:743-748(1998).
RA [16]
RA VARIANT VAL-473:
RA MEDLINE=21143723; PubMed=11245641;
RA Wu K.K., Alekic N., Ahn C., Boerwinkle E., Polson A.R.,
RA Junega H.,
RA "Thrombomodulin Ala45Val polymorphism and risk of coronary heart
RA disease.",
RA Circulation 103:1386-1389(2001).
RA [17]
RA FUNCTION: THROMBOMODULIN IS A SPECIFIC ENDOTHelial CELL RECEPTOR
RA THAT FORMS A 1:1 STOICHIOMETRIC COMPLEX WITH THROMBIN. THIS
RA COMPLEX IS RESPONSIBLE FOR THE CONVERSION OF PROTEIN C TO THE
RA ACTIVATED PROTEIN C (PROTEIN CA). ONCE EVOLVED, PROTEIN CA
RA SCISSIONS THE ACTIVATED COFACTORS OF THE COAGULATION MECHANISM,
RA FACTOR VA AND FACTOR VIIIa, AND THEREBY REDUCES THE AMOUNT OF
RA THROMBIN GENERATED.
RA [18]
RA SUBCELLULAR LOCATION: Type I membrane protein.
RA [19]
RA TISSUE SPECIFICITY: ENDOTHELIAL CELLS ARE UNIQUE IN SYNTHESIZING
RA THROMBOMODULIN.
RA [20]
RA POLYMORPHISM: VARIATIONS IN THBD ARE ASSOCIATED WITH AN INCREASED
RA RISK OF DEVELOPING THROMBOEMBOLIC DISEASES (TED).
RA [21]
RA DISEASE: DEFECTS IN THBD COULD BE THE CAUSE OF INHERITED TED,
RA ALSO CALLED INHERITED THROMBOPHILIA. PATIENTS WITH TED HAVE
RA DEFECTS OF THE HAEMOSTATIC SYSTEM WHICH CREATES A TENDENCY TO THE
RA OCCURRENCE OF THROMBOSIS. TED PLAY AN IMPORTANT ROLE IN THE
RA PATHOGENESIS OF VARIOUS CARDIOVASCULAR DISORDERS.
RA [22]
RA SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
RA [23]
RA DATABASE: NAME=PROW; NOTE=CD guide CD141 entry;
RA WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd141.htm".
RA [24]
RA This SWISS-PROT entry is copyright. It is produced through a collaboration
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RA or send an email to license@isb.slb.ch).
RA [25]
RA EMBL: X05495; CAA29045.1;
RA EMBL: M16552; AAB59508.1;
RA EMBL: J02973; AAA61175.1;
RA EMBL: D00210; BAA00149.1;
RA EMBL: AL049651; CAB51954.1;
RA PIR: A27073; A27073.
RA PIR: A28307; A28307.
RA PIR: A29680; A29680.
RA PIR: IEGR; 15-NOV-95.
RA PDB: 1FGD; 20-JUN-96.
RA PDB: 1FGR; 08-JUN-96.
RA PDB: 1ZAO; 29-JAN-96.
RA PDB: 1ADY; 24-DEC-97.
RA PDB: 2ADY; 24-DEC-97.
RA GlycoStatedb: P07204;
RA MIM: 188040;
RA InterPro: IPR000152; Asy hvdrftrv]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2002, 09:33:56 ; Search time 30.72 Seconds

(without alignments)
2759.359 Million cell updates/sec

Title: US-09-902-713B-96

Perfect score: 2605

Sequence: 1 MRPAFALCLIMQALWPGPG.....LRDRAEGALLAESPLGSSDA 490

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Database :

1: SPTREMBL.19:.*
2: SP_Bacteria:.*
3: SP_Fungi:.*
4: SP_Human:.*
5: SP_Invertebrate:.*
6: SP_Mammal:.*
7: SP_Mhc:.*
8: SP_Organelle:.*
9: SP_Phage:.*
10: SP_Plant:.*
11: SP_Protoct:.*
12: SP_Virus:.*
13: SP_Vertebrate:.*
14: SP_Unclassified:.*
15: SP_Virus:.*
16: SP_Bacteriaph:.*
17: SP_Archaea:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1586.5	60.9	459	11 09D624	09d624 mus musculu
2	1584.5	60.8	459	11 09CXAB	09cxa8 mus musculu
3	1574.5	60.4	459	11 09DC55	09dc55 mus musculu
4	957.5	36.8	212	4 09P096	09p096 homo sapien
5	350	13.4	757	4 09HC00	09hcu0 homo sapien
6	336.5	12.9	765	11 091ZV1	091zv1 mus musculu
7	336.5	12.9	765	11 091V98	091v98 mus musculu
8	309	11.9	652	4 09NPY3	09npv3 homo sapien
9	307	11.8	652	4 000274	000274 homo sapien
10	305	11.7	643	11 09U126	09u126 rattus norv
11	303	11.6	644	11 089103	089103 mus musculu
12	301	11.6	643	11 09ET61	09et61 rattus norv
13	227	8.7	468	4 09UC32	09uc32 homo sapien
14	193	7.4	577	11 035370	035370 rattus norv
15	143.5	5.5	184	4 09HCY3	09hcy3 homo sapien
16	142	5.5	955	4 096DN2	096dn2 homo sapien

17	139.5	5.4	273	11 09CXMO	09cxm0 mus musculu
18	139	5.3	461	11 P97883	P97883 rattus norv
19	139	5.3	1394	5 09VS89	09vs89 drosophila
20	138.5	5.3	443	4 09H3D5	09h3d5 homo sapien
21	137	5.3	1637	6 09XSV8	09xsv8 bos taurus
22	135.5	5.2	624	4 096JG5	096jg5 homo sapien
23	133.5	5.1	443	4 096TF5	096tf5 homo sapien
24	132.5	5.1	443	11 09JMO6	09jmo6 mus musculu
25	132.5	5.1	1238	4 09UE99	09ue99 homo sapien
26	132.5	5.1	1238	4 09E600	09e600 homo sapien
27	132.5	5.1	1238	4 09UNE8	09un8 homo sapien
28	132.5	5.1	1238	4 09UE17	09ue17 homo sapien
29	132	5.1	3507	5 023587	023587 caenorhabd
30	131.5	5.0	1238	4 09Y219	09y219 homo sapien
31	130.5	5.0	985	12 067643	067643 gallid hep
32	129.5	4.9	1106	5 017494	017494 caenorhabd
33	128.5	4.9	803	6 09GWF9	09gmt9 macaca fasc
34	128.5	4.9	1001	4 09BYH8	09byh8 homo sapien
35	128.5	4.9	1404	5 09VB65	09vb65 drosophila
36	124.5	4.8	2809	4 096UP8	096up8 homo sapien
37	123	4.7	1200	4 09E6P9	09e6p9 homo sapien
38	122.5	4.7	374	4 096NF3	096nf3 homo sapien
39	122.5	4.7	374	4 096NC5	096nc5 homo sapien
40	122.5	4.7	1479	11 064449	064449 mus musculu
41	122.5	4.7	2319	11 09R172	09r172 rattus norv
42	122	4.7	248	11 09Z211	09z211 mus musculu
43	122	4.7	1963	6 028019	028019 bos taurus
44	122	4.7	2471	11 09QW30	09qw30 rattus sp.,
45	121.5	4.7	374	11 09Z209	09z209 cricetulus

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	459 AA.
Q9D624	Q9D624			
AC	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	1200003C23RIK PROTEIN.			
GN	1200003C23RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=HEAD;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann M., Gaasterland T., Giesi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,			
RA	Blake J., Boilell D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,			
RA	Hashizaki Y.,			
RT	*Functional annotation of a full-length mouse cDNA collection.*;			
RT	Nature 409:685-690(2001).			
EMBL	AK014681; BAB2502.1; -			
DR	HSSP; P00743; ICCF.			

01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE 1200003C23RIK PROTEIN.
EN 1200003C23RIK.

RP SEQUENCE FROM N.A.
 RX MEDLINE-21269274; PubMed-11084048;
 RA Christian S., Ahorn H., Koehler A., Eisenhaber F., Rodi H.P.,
 RA Garin-Chesa P., Park J.E., Ketting W.J., Lenter M.C.,
 RT "Molecular cloning and characterization of Endostalin, a C-type
 lectin-like cell surface receptor of tumor Endothelium.",
 RL J. Biol. Chem. 276:7408-7414(2001).
 DR EMBL; AF279142; AAG00867.1;
 DR EMBL; AJ295846; CAC34381.1;
 DR HSSP; P07204; I2A0;
 DR Interpro: IPR000152; Asx_hydroxyl.
 DR Interpro: IPR000561; EGF-like.
 DR Interpro: IPR001861; EGF-like.
 DR Interpro: IPR001304; lectin_c.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00059; lectin_c.1.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00181; EGF; 3.
 DR SMART; SM00179; EGF_CA; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KM Signal.
 FT SIGNAL.
 FT CHAIN.
 SQ SEQUENCE 757 AA; 80858 MW; C96363EALFBEFFAO CRC64;

Query Match 13.4%; Score 350; DB 4; Length 757;
 Best Local Similarity 26.1%; Pred. No. 2,8e-20;
 Matches 122; Conservative 44; Mismatches 147; Indels 154; Gaps 20;

QY 7 LCLIMQALMPGGGGGHPHTA--DIAGCSAGACYSLSHATMKROAEACILRGALSTV 64
 DB 5 LLLMAA--AGPTLGDPMAEPRAACGPS--SCYALPPRRRTFLEAARACREIGDLATP 61
 QY 65 RAGALRAVALALRAGPGGGGSKDLFWVALERRRSHCTLENPLRGFWLSSDGGLE 124
 DB 62 RTPEAQRVDSLVGAGA-----SRLMIGLQROAQCO--RPLNGFTWTGD----- 109
 QY 125 SDT--LOWVEEPQRS--CTARCAVLAQTGVEPAGKEMKCHLRANGYLCKYFYLCPA 181
 DB 110 QDTAFWMAQPGAGGCPAPARCVALEASG---EHRMLESGCTLAVGYLQGFEGEACRA 166
 QY 182 --PRPGAASNLSTYRAPOLHSALDFSPGTEVSALCRGLPISVCIAD--ELGANW--- 235
 DB 167 LDPAAGAGAVYTPPHLVSTFEWLPFGSAVAOCQAGRGASLLCVKQPEGVMSRA 226
 DB 236 -----DKLSGVDLQPCPGRYLRAG-----KCAELP----- 260
 DB 227 GPLCLGTGSGPDNGGCEHECEVEVDGHVSCRCETGFRILADGSCDPAQAPCEQCEP 286
 QY 261 -----NCLDDLGGFACCATGFELEND 282
 DB 287 GGPQGSCHCRIGFRAEDDPHRCVDTDCQIAGVCOQCMVYVGFECEYCEGHELEAD 346
 QY 283 GRSCVTSGE-----GQPTL-----GGTVVP-----TRRPAT 309
 DB 347 GISCSFAGAMGAQASQDLDELDDGEDEDEDEAMKAFNGWTEPGLIMEPTQPDF 406
 QY 310 AYS-----PVQRTWPIRVDEKIGETPLVVEQDNSVTSI 343
 DB 407 ALAYRSPEDREPOLPYPEPTWPPPL-----SABRVP--YHSSVLSV 447

RESULT 6
 0912V1
 AC 0912V1 PRELIMINARY; PRT; 765 AA.
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ENOCSTALIN.
 GN TEM1.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SWISS WEBSTER; TISSUE=THYMUS;
 RX MEDLINE-21486432; PubMed-11489895;
 RA Opavsky R., Havliernik P., Jurkovicova D., Garin M.T., Copeland N.G.,
 RA Gilbert D.J., Jenkins N.A., Bies J., Garfield S., Pastorekova S.,
 RA Que A., Wolff L.,
 RT "Molecular Characterization of the Mouse Tem1/endostalin Gene
 Regulated by Cell Density in Vitro and Expressed in Normal Tissues in
 Vivo."
 RL J. Biol. Chem. 276:38795-38807(2001).
 DR EMBL; AF388572; AAK84664.1;
 SQ SEQUENCE 765 AA; 81823 MW; 07B3225E5DD13A03 CRC64;

Query Match 12.9%; Score 336.5; DB 11; Length 765;
 Best Local Similarity 32.8%; Pred. No. 3.6e-19;
 Matches 94; Conservative 33; Mismatches 133; Indels 27; Gaps 12;

QY 7 LCLIMQALMPGGGGGHPHTADRAGCSAGACYSLSHATMKROAEACILRGALSTVRA 66
 DB 5 LLLMAA--AGPTLGDPMAEPRAACGPS--SCYALPPRRRTFLEAARACREIGDLATP 63
 QY 67 GAEALRAVALALRAGPGGGGSKDLFWVALERRRSHCTLENPLRGFWLSSDGGLESD 126
 DB 64 PEAQRVDSLVGAGANG-----LWIGLQROAQCO--PQPLNGFTWTGD-----QD 111
 QY 127 T--LOWVE--EPORSTARCAVLAQTGVEPAGKEMKCHLRANGYLCKYFYLCPA-- 181
 DB 112 TAFWMAQPGAGGCPAPARCVALEASG---EHRMLESGCTLAVGYLQGFEGEACRA 168
 QY 182 PRPGAASNLSTYRAPOLHSALDFSPGTEVSALCRGLPISVCIADET--GANWKLSG 240
 DB 169 LEVGAAGAVYTPPHLVSTFEWLPFGSAVAOCQAGRGASLLCVKQPEGVMSQTG- 227
 QY 241 DVLCCPGRYLRAGKCAELPNCDDL--GGFACCATGFELEKDRSC 286
 DB 228 PLCPGTGCGPDNGGCEH--ECVEEVDGAVSCRCSEGRILADGHS 271

RESULT 7
 091V98
 AC 091V98 PRELIMINARY; PRT; 765 AA.
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE TUMOR ENDOTHELIAL MARKER 1 PRECURSOR (ENDOSTALIN).
 GN TEM1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=21443268; PubMed-1159528;
 RA Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
 RA Kinzler K.W., St Croix B.,
 RT "Cell surface tumor endothelial markers are conserved in mice and
 humans."
 RL Cancer Res. 61:6649-6655(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=12956/SVEVTA; TISSUE=SPLEEN;
 RX MEDLINE-21486432; PubMed-11489895;
 RA Opavsky R., Havliernik P., Jurkovicova D., Garin M.T., Copeland N.G.,
 RA Gilbert D.J., Jenkins N.A., Bies J., Garfield S., Pastorekova S.,
 RA Que A., Wolff L.,
 RT "Molecular Characterization of the Mouse Tem1/endostalin Gene

RT Regulated by Cell Density in Vitro and Expressed in Normal Tissues in
 RT Vivo.
 RL J. Biol. Chem. 276:38795-38807(2001).
 DR EMBL: AF378758; AAL11995.1;
 DR EMBL: AF388573; AAK8465.1;
 KM Signal.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 765 TUMOR ENDOTHELIAL MARKER 1.
 SQ SEQUENCE 765 AA; 81813 MM; 572A06CC15BC8C8 CRC64;

Query Match 12.9%; Score 336.5; DB 11; Length 765;
 Best Local Similarity 32.8%; Pred. No. 3,6e-19;
 Matches 94; Conservative 33; Mismatches 133; Indels 27; Gaps 12;

QY 7 LCLLQALMPGCGGGEHPADRGCSAGACYSLSHATMKROAAEEACILRGALSTVRA 66
 DB 5 LLLAAVAVPALGQVPMPEPRAACPS-SCYALPFRRTFLAMKACELGSLATPPT 63
 QY 67 GAELEAVLALRAGPGGGSKDLFWALERRSHCTLENEPLRGFSWLSDDPGLESD 126
 DB 64 PEARAVSLVGVGANG-----LLMIGLQROARCCQ-POBPLRGFIWTTGD-----OD 111
 QY 127 T-LQWVE-EPQRCSTARCAVLQATGVEPAGKEMRCHLANGYLCKYQEVLCQA-- 181
 DB 112 TAFTHAQATGCPGPAQKCALERSG---EHRMLEGSCITLAVDGLCPGEGACPALP 168
 QY 182 PRPGAASNLSTYRAPPOLHSAALDFSPPTGVSALRGQPLISVTCIADBI-GARMDKLSG 240
 DB 169 LEVGQAGPAVYTPFNVLVSSEFEMLPFQSVAAVQCAAGSALICVKQSGGWSQGTG- 227
 QY 241 DVLCPGPGYTLAAGKCAELPCLDLI-GGFACECATGFLGKDGNSC 286
 DB 228 -PLCGTGGCGPNDGCGE--ECVEEYDGAVSCRCSEGFRLADGHSC 271

RESULT 8
 ID Q9NPY3 PRELIMINARY; PRT; 652 AA.
 AC Q9NPY3;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE DJ737E23.1 (COMPLEMENT COMPONENT C1Q RECEPTOR).
 GN DJ737E23.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sehra H.;
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AL118508; CAC00597.1;
 DR HSSP: P35555; IEMN.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001304; Iectin_C.
 DR Pfam: PF00008; EGF_5.
 DR SMART: SM00034; CLECT; 1.
 DR SMART: SM00179; EGF_CA_3.
 DR SMART: SM00001; EGF_Like; 2.
 DR PROSITE: PS00010; ASX_HYDROXYL; 3.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS01187; EGF_CA; 3.
 KM Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
 KW Receptor; Repeat.
 SQ SEQUENCE 652 AA; 68560 MM; EECADPEAC55FCAC2 CRC64;

Query Match 11.9%; Score 309; DB 4; Length 652;

Best Local Similarity 21.4%; Pred. No. 5,3e-17;
 Matches 139; Conservative 82; Mismatches 205; Indels 224; Gaps 28;

QY 1 MRPAFALCLLQALMPGCGGGEHPADRGCSAGACYSLSHATMKROAAEEACILRGGA 60
 DB 1 MATSMGLILLILLITLQPGAGTADTEAVYCVGT-ACVTAHSGKLSNAEONHCNONGN 59
 QY 61 LSTVRAGAE--LRAVLA--LLRAGPGGGSKDLFWALERRSHCTLENEPLRGFSW 115
 DB 60 LATVKSKEEAQHVQVLAQLLRREALTLARMSK---FWIGLQREKCKCLDPSLPLGFSW 116
 QY 116 LSSDPGLESIDLQWVEPQRCSTARCA--VLQATGVEPA--GWKEKRC-----HL 164
 DB 117 VG--GGEDTPYSNMWKEKLNCSIKRCVSLDLISQPLPSRLPWSSEGPCSPSPGS 173
 QY 165 RANGYLCCKQFVLCAPRPGAASNLSTYRAPPOLHSAALDFSPPTGVSALRGQPLIS 214
 DB 174 NIEGFVCKFSFKMCRPLALGSGQVYTTTFPTTSSLEAVFAANAVAGEGKDET 233
 QY 215 ----LCRGQLP-----ISVTCIADIGARD-----RL 238
 DB 234 QSHYFLCKEKAPDVPDMSSGPLCVSPKYGCMFNNGCHODCFEGDGSFLCGRPGFRL 293
 QY 239 SGDYLV-----CCCPGRY-----LRGKCAELP 260
 DB 294 LDDLVTGCASRNPCSSPPCRGATCYLGHGKNYTCRCPOGYQLDSSQLDCVDVDECQDSP 353
 QY 261 ---NCLDDLGFCACATGFE-----278
 DB 354 CAQECVNTQGFGECEWVGEPGPGEGACQDVDECALGRSPAQCCTNIDGSFHCSE 413
 QY 279 ----LCKDGRSC---VTSGECP-----TLGCTGVPTRPPAT 309
 DB 414 GYVLAGEDEITQCQDVDECVPGGRLCDSLCFNTQGSFHCCLPGWVLAIPGVYCTMGPSV 473
 QY 310 ATSPVQRTWPIRYD--EKIGETPLVPEQDINSVTSIP-ELPRKSGSSTSLQMSIQAES 366
 DB 474 LGPPSGP---PDEEDGEKEGST--VP---RAATVASTPRTGECTPAPATYTSRSLSSDA 525
 QY 367 KAT-----ITPSSG-----VISKFNSTTSATQAQDSSA-----VVEF 401
 DB 526 PITSALKLMLAPSGSCGVAREPSIHHTAASQPGERAGDSSVAATQNNQDQKLLFY 585
 QY 402 EVSTAVVAVILTMVLGLVKLCFHESPSSQPRKESMGPPGLESDEPPAA 451
 DB 586 ILGTVAAILLLAL-ALGL--LVYRRRRRAKREKK-----EKKPQNA 625

RESULT 9
 ID Q00274 PRELIMINARY; PRT; 652 AA.
 AC Q00274;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE C1QR(P).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97199258; PubMed-9047234;
 RA Neomuceno R.R., Henschen-Edman A.H., Burgess W.H., Tenner A.J.;
 RT cDNA cloning and primary structure analysis of C1QR(P), the human
 RT C1q/MBL/SPA receptor that mediates enhanced phagocytosis in vitro.";
 RT Immunity 6:119-128(1997).
 DR EMBL: U94333; AAB3110.1;
 DR HSSP: P35555; IEMN.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001304; Iectin_C.

DR Pfam: PF00008; EGF, 5.
 DR Pfam: PF00059; lectin_c, 1.
 DR SMART: SM00034; CLECT, 1.
 DR SMART: SM00179; EGF_CA, 3.
 DR SMART: SM00001; EGF_Like, 2.
 DR PROSITE: PS00010; ASX_HYDROXYL, 3.
 DR PROSITE: PS00041; C_Type_Lectin_2, 1.
 DR PROSITE: PS01186; EGF_2, 3.
 DR PROSITE: PS01187; EGF_CA, 3.
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 SO SEQUENCE 652 AA; 68577 MW; B7BAB5E5714A75 CRC64;

Query Match 11.8%; Score 307; DB 4; Length 652;
 Best Local Similarity 21.4%; Pred. No. 7.7e-17;
 Matches 139; Conservative 81; Mismatches 206; Indels 224; Gaps 28;

1 MRAFAALCLLMQALMPGGGEGHPADAGCSASGACSLHATMKROAEACILRGGA 60
 1 MATSKMLLLLLLTLOPAGTAGADTEAVVCGT-ACYTAHSGKLAAEAQNHQNGN 59
 61 LSTVRAGAE--LRVLA--LIRAGPGGGSKDLLFWALERRSHCTLENEPLRGFSW 115
 60 LATVSKKEPAOHVQVLAQOLLRREALIARMSK--FWIGLOREKGLDSEPLKGSW 116
 116 LSSDGLSEDTLOWVEEPONSCTARRCA--VLATGVEP--AGKEMRC-----HL 164
 117 VG--GGEDTPYSNMHKLRLNSCLSKRCVSLDLISPLLPNRLPKHSEGGSGSPSGS 173
 165 RANGYLCKYQFEVLCPPARPAASNLRYRAPFOLHSAALDSPGTEVSA----- 214
 174 NIEGVCFKFSKGMCRPLALGPGQVITTFPOTTSSLEAVPPASANAACGGKDET 233
 215 --LCGQLP-----ISVCTADEIGARWD-----KL 238
 224 QSHFLCKEKAPDVEFDGSSGSLCVSPKYGCFNNGGCHODCEGSGSLCCGRGFR 233
 239 SGDVLT-----CPRGRY-----LRAGKCAELP 260
 294 LIDLVTCAARNPCSSPCRGATVLCPRHKNYTCRCRCPQGLDSSQLDVCVDDECODSP 353
 261 --NCUDDLGFCACATGFE----- 278
 354 CAQECVMPGFCRCCEWVGEPGPGEGACQDVECALGSPCAQCGTNTDGSFHCSE 413
 279 --LGRDGRSC--VTSGEGOP-----VLGTVTRRPAT 309
 414 GYVLAGEGDTQCQDVECVPGGFLCDSLCFNQGSGFCGLPGWVLAENGVSCTMGPS 473
 310 ATSPVQRTPIRVD--EKLGTPLVPEODNSTYVIP-ELPRWGSOSTSTLQMSLOAES 366
 474 LGPPSGP--PDEEDGKEKRGST--VP--RATASPTGREGTPEKATPTTSRPLSSDA 525
 367 KAT-----ITPSGS-----VISKFNSTTSATPQAFDSSA-----VVEFI 401
 526 PITSAPLKLAPAGSSGVNREPSSIHATTAASGPQEPAGDSSAVANONNGTQKLLIFY 585
 402 FVSTAVVAVILMTVLGLVKLCFHESSSPRKESMPGGLSEDEPA 451
 586 ILGTVAAILLAL-ALGL-LVYKRRRAKREK-----EKKPQNA 625

RESULT 10
 09J126 PRELIMINARY; PRT; 643 AA.

AC 09J126; 01-OCT-2000 (Tremblrel, 15, Created)
 DT 01-OCT-2000 (Tremblrel, 15, last sequence update)
 DE 01-DEC-2001 (Tremblrel, 19, last annotation update)
 GN C10BP
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTER; TISSUE=LUNG;
 RX MEDLINE=20507883; PubMed=10934210;
 RA Dean Y.D., McGreal E.P., Akatsu H., Gasque P.
 RT "Molecular and Cellular Properties of the Rat A4 Antigen, a C-type
 lectin-like Receptor with Structural Homology to Thrombomodulin.";
 RL J. Biol. Chem. 275:34382-34392(2000).
 DR EMBL: AF160978; AAF0402.1;
 DR HSSP: P35355; IEMN.
 DR Interpro: IPR000152; Asx_hydroxy1.
 DR Interpro: IPR000561; EGF-like.
 DR Interpro: IPR001881; EGF_CA.
 DR Interpro: IPR001304; lectin_c.
 DR SMART: SM00034; CLECT, 1.
 DR SMART: SM00179; EGF_CA, 3.
 DR SMART: SM00001; EGF_Like, 2.
 DR PROSITE: PS00010; ASX_HYDROXYL, 3.
 DR PROSITE: PS00041; C_Type_Lectin_2, 1.
 DR PROSITE: PS01186; EGF_2, 3.
 DR PROSITE: PS01187; EGF_CA, 3.
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
 SO SEQUENCE 643 AA; 68780 MW; FB23D742B02A4931 CRC64;

Query Match 11.7%; Score 305; DB 11; Length 643;
 Best Local Similarity 20.8%; Pred. No. 1.1e-16;
 Matches 129; Conservative 66; Mismatches 185; Indels 240; Gaps 23;

7 LCLLMQALMPGGGEGHPADAGCSASG-ACYSLHATMKROAEACILRGALSTVR 65
 11 LGLLQ-LMAG-----AAADSEAVVCEGTACTAYAHWKLAAEAQNRCHNNGSNLAVK 63
 66 AGAELRAV--LALRAPPGGGSKDLLFWALERRSHCTLENEPLRGFSWISDPG 122
 64 SEEARHVOEALQILTKRAP-SETKIGKFWIGLOREKGTCTYHDLPMKFSWVG-- 119
 123 LESDTLOWVEEPONSCTARRCAVLQATGVGP--AGKEMRCNL--RANGYL 171
 120 EDTTYSNMVYKSKSSCLSKRCVSLDLISLKPSPHSHLPKHESPCGTPDAPGNSIGFLC 179
 172 KYQEVLCPPARPAASNLRYRAPFOLHSAALDSPGTEVSAIC----- 216
 180 KFNKGMSPALAGPQGLYITTFPQATTSKLAAPASAVANVCGDEAESKTYILKE 239
 217 --RGQLPIS-----VTGIA 228
 240 TTAGVFNHSGSLPCLVSPKFGCSFNNNGCCQDCEGSGSFRGCGRPRLLDLVTQAS 299
 229 ----- 228
 300 RNPSSNPCTGGGCMGHSVPLENITGHCPRGYQLDSSVHCVDIDCEDSPCDQECINP 359
 229 -----DELGARWD-----KLSDVLCPCPGRTIARGR----- 255
 360 GGFHCEGCMVGYSSGSEACEEDVDECTAAYSPCAAGCINTDGSFCSCKEYITMSGKS 419
 256 --CAELPNCI--DDL--GFCACATGPELCKDRSCVTSGEGPTLGG--TGVP 302
 420 TQCEDIDECIAGNCDITLCINTDGSFRCGCPAGFETLAPNVSC-----TRGSFSELP 471
 303 TRRPATATSPVQRTPIR-----VDENKLGTPLVPEODNSTYVIPETPRGKS 351
 472 ARPPQKEDKGDKESTVPLTEMPGSLNGSKDVSNNAQTITDLSIOSSSTASVP----- 524
 352 QSTMSTLQMSLOAESK-----ATTSPGSVTSKFNSTTSATPQAFDSSS--AVVEFI 401
 525 -----LEIEVSSSEADSVWLDIGTYLPTTSGHSQ--PTHEDSVPAHSDSDIDGKLLIFY 576
 402 FVSTAVVAVILMTVLGLV 421

Query Match 11.6%, Score 301, DB 11, Length 643;
 Best Local Similarity 20.6%, Pred. No. 2,3e-16;
 Matches 128; Conservative 67; Mismatches 185; Indels 240; Gaps 23;

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OY 7 TLLMOLMPGPGGGEHPTADRAGCSAG-ACYSLHHTMKROAEACILRGSLSTVR 65
DB 11 LGLLGO-LWAG-----AAOSEAVVCEGTACTYTHMKGLSAAEOKHRCNENGMATYK 63
OY 66 AGAEIRAV---LALLRAGPGGGSKDLFWALEERRSHOCTLENEPLRGESWLSDDGG 122
DB 64 SEEARHVOEALQDLTKRAP-SETKICKFMTGLORREKCKCTYHDLPMKGFSSWG--GG 119
OY 123 LESDLOWEEFORCTARRCAVLQATGVPE--AGKEMRHL-----RANGVLC 171
DB 120 EDTTSMNYKASKSCISCKRCVSLIDLSTKPHSHLPKMHESPCTGPDADGNSTEGFLC 179
OY 172 KYQEVLCPADRPGASMSLYRAPFOLHSAALDESPGTEVSALC-----216
DB 180 KFNFKMGCSPLALGPGGLTFTTPOATTSILKAVPFAVSANVOCGDEAKETNYLCKE 239
OY 217 -----RGOLPIS-----VTCIA 228
DB 240 TTAGVFHFGSSGGLVCEVFKFCGCSFNNNGCQDCEGGDGSFRCGRFRLLDLVTCAS 299
OY 229 -----228
DB 300 RNPSSNPTCGGGMCHSVPLSENTHCHPRGYOLDSQVHVDIDECEDSCDECIINTP 359
OY 229 -----DELGARD-----KLSDVLCPCPCRYLRAG--254
DB 360 GGFHCEWGVYOSGSGSEACEVDCTAAYSPCAQCTINTDGSFYSCKEGYIMSGEDS 419
OY 255 -KCAELNCL---DDL-----GGFACECATGFELKDGSCVYSGSGQPLTG--TGV 302
DB 420 TCCEDIDECIGNPCDYLICINTDGSFRCGAGFELAPNGVSC-----TRGSMFELP 471
OY 303 TRRPATATSPVQRTPIR-----VDEKLEETPLVPQDMSVTSIPEIPRWGS 351
DB 472 ARPQKEDKDGKESTVPLEMPGLNSKDVSNRAQTDLISQSDSTASVP-----524
OY 352 QSTWSTLMSLOESK-----ATTPSGVISKFNSTTSATPOANDSS--AVFT 401
DB 525 -----LEIVSSPASVWMLDLGTYLPTTSGHSQ--PTHEDSVPAHSDSDTDQKLLFY 576
OY 402 EVSTAVVAVILMTVVLGV 421
577 ILGTVAISILLAL-ALGIL 595

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RESULT 13

09UC32 PRELIMINARY; PRT; 468 AA
 AC 09UC32;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE THROMBOMODULIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE.
 RA MEDLINE=93293792; PubMed=8390446;
 RA Yamamoto S., Mizoguchi T., Tamaki T., Onkuchi M., Kimura S., Aoki N.,
 RT "Urinary thrombomodulin, its isolation and characterization.",
 RL J. Biochem. 113:433-440(1993).
 DR HSSP; P07204; 1ZAO.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR001491; Thrombomodulin.
 DR Pfam; PF00008; EGF; 4.
 DR Pfam; PF00059; Lectin_C; 1.
 DR PRINTS; PR00907; THROMBOMODULN.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00181; EGF; 6.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 DR PROSITE; PS01186; EGF 2; 2.
 DR PROSITE; PS01187; EGF_Ca; 1.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat
 SO SEQUENCE 468 AA; 49444 MW; 4BFEBE98EF86A40 CRC64;

Query Match 8.7%, Score 227, DB 4, Length 468;
 Best Local Similarity 25.7%, Pred. No. 1.9e-10;
 Matches 85; Conservative 36; Mismatches 120; Indels 90; Gaps 18;

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OY 16 PGEGGEHPTADRAGCSAGSACYSLHHTMKROAEACILRGALSTVRAGAEIRAVIA 75
DB 5 POGSGQCVCHD-----CEALYCPATFPLNASQICDGLRGLMTYSSVAADVISI 55
OY 76 LIRAGPGGGSKDLFWALE-----RRSHOCTLENEPLRGESWLSDDPGLESDT 127
DB 56 LIN---GDGSGVRRL-WIGQLPCCGDPKRLG-----PLRGFWYTGDNNTSYS--102
OY 128 LOWEERORS-----CTARRCAVLQATGVPEAPGKMKERHLRANGVLCYQEVLC 180
DB 103 -RWARLDLNPALPGPLCAVNSAA--EATVSPPI-WEQQCEYKADGELCEHFPATQR 158
OY 181 -APRGAAS--NLSTYRAPFOLHSAALDESPGTEVSALCRQLPISTCIAD-----229
DB 159 PLAVEFGAANAAYSTIYGFPAARGADFOALPVGSSAAV--APGLQIMCTAPGAVOG 215
OY 230 -----EIGARD-----KLSDVLCPCP-----GRLRAG--KCAEL--259
DB 216 HWAREAPGAMDCVENGGEHACNAIPGAPRCOCPRGALLOADGRCTASATQSCNDLCE 275
OY 260 -----PNCIDDLGCFACECATGFELKDGGRSC 286
DB 276 HFCVFN-PPQPSYSQMCCTGYRLADQHRG 305

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RESULT 14

035370 PRELIMINARY; PRT; 577 AA.
 AC 035370;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE THROMBOMODULIN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LUNG;
 RA Wang J., Yao A., Wang J.Y., Hardin J.W., Hauer-Jensen M.,
 RL Submitted (Sep-1997) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 1-136 FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Yao A., Wang J., Hardin J.W., Hauer-Jensen M.,
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF022743; AAB80760.1;
 DR EMBL; AF022742; AAB80923.1;
 DR HSSP; P07204; 1EGD.
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 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001304; Lectin_C.

DR InterPro: IP0001491; Thrombomodulin.
 DR Pfam: PF00008; EGF_5.
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 DR PRINTS: PR00907; THROMBOMODULN.
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 QY 97 ERRRSNC--TLENPEPLRGFWLSSDPGGLESPTLQWVEEPORS-----CTARCAVLQ 147
 DB 89 QLPQG--CGDPVHLGLPLGFGQWVTGDN--HTSYSRMARPDQSPPLCGPLCVTSTATEA 144
 QY 148 ATGVEPAGKEMKCHLRANGYLCKYQFEVLCAPAPR-----GAASNLSTYRAPEQL 198
 DB 145 APG--EPA--WEKPCENETGFLCEFEFAFC---RLRNTRNDPEAHISSTNTPLGV 198
 QY 199 HSAALDFSPGTEVSA-----LCR-----GQLPISVT---CIADEIGARW--DKL 238
 DB 199 SGADFQTLPIGSSATVAPFGLIEVLCRALPQTSSEGHMTREVTGAMNCSEVNGCCYMCNR 258
 QY 239 SGVILPCP--GRTLR--GK-----CAEL-----PNCLLDLSGFACGATGFEIGKD 282
 DB 259 ANGPVCVPGSGDLQADGRCACPVADLCNELCOHFCVNNSDVPGSYSCMCETGYOLAAD 318
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 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
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 GN PRED12.
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
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 RA Lehrach H., Reinhardt R., Yaspo M.L.;
 RA Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
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 DR Pfam: PF00059; lectin_c; 1.
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 QY 92 FWALERRRSHCTLENPEPLRGFWLSSD--PGLESPTLQW-----VEEPORS 137
 DB 72 FWIGL-----WRNGDQGTSGACPDLYQWSDGNSQYRMWYDDEP--S 111
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Search completed: August 13, 2002, 09:37:54
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Tue Aug 13 09:56:31 2002

us-09-902-713b-96.rspt

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2002, 09:34:26 ; Search time 34.18 seconds
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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1	490	100.0	490	20	AAV13360		Amino acid sequenc	
2	490	100.0	490	21	AAB33460		Human PRO269 prote	
3	490	100.0	490	21	AAB24403		Human PRO269 prote	
4	490	100.0	490	21	AAV95016		Human secreted prot	
5	490	100.0	490	22	AAU12349		Human PRO269 poly	
6	490	100.0	490	22	AAE06596		Human protein hav	
7	296	60.4	331	21	AAB41847		Human ORFX ORF1611	
8	274	55.9	344	21	AAV91410		Human secreted pro	
9	242	49.4	428	22	AAB80228		Human PRO269 prote	
10	139	28.4	175	21	AAV95031		Human clone vp15.1	
11	84	17.1	189	21	AAV91349		Human secreted pro	

[illegible]

85	7	1.4	144	22	AAU56983	Propionibacterium
86	7	1.4	147	22	AAU41537	Propionibacterium
87	7	1.4	147	22	AAU87796	Human immune/haema
88	7	1.4	148	22	AAU01882	Human polypeptide
89	7	1.4	153	21	AAU65656	Propionibacterium
90	7	1.4	159	21	AAU14119	Human secreted pro
91	7	1.4	159	22	AAU85241	Human secreted pro
92	7	1.4	177	22	AAU09342	Novel human diago
93	7	1.4	218	12	AAU11000	Antigenic peptide
94	7	1.4	229	21	AAU41733	Human ORFX ORF197
95	7	1.4	238	10	AAU93696	Antigenic polypept
96	7	1.4	244	22	AAU32672	Novel human secret
97	7	1.4	246	22	AAU58306	Novel human secret
98	7	1.4	267	21	AAU52135	Propionibacterium
99	7	1.4	288	21	AAU27461	Arabidopsis thalia
100	7	1.4	290	22	AAU12645	Novel human diago
101	7	1.4	291	22	ABG20856	Novel human diago
102	7	1.4	303	22	AAU81311	Human AFP protein
103	7	1.4	312	21	AAU43256	Human ORFX ORF3020
104	7	1.4	319	17	AAU00628	Protein kinase #1
105	7	1.4	320	22	AAU61055	Drosophila melanog
106	7	1.4	330	20	AAU66020	Human homeobox gen
107	7	1.4	332	22	AAU72076	Human olfactory re
108	7	1.4	333	20	AAU86019	Murine homeobox HO
109	7	1.4	333	22	ABG19326	Novel human diago
110	7	1.4	336	20	AAU63635	TANGO 300 signal-1
111	7	1.4	341	22	AAU19442	Human diagnostic p
112	7	1.4	346	22	AAU1462	Human cancer assoc
113	7	1.4	353	21	AAU43736	Human colon cancer
114	7	1.4	353	22	AAU37374	Drosophila melanog
115	7	1.4	359	22	ABU66298	Human secreted pro
116	7	1.4	361	21	AAU23618	Human AFP protein
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118	7	1.4	361	22	AAU61421	Human TANGO 300 pr
119	7	1.4	384	22	AAU99127	Human G protein-co
120	7	1.4	384	22	AAU66727	Human 16405 protei
121	7	1.4	386	22	AAU79926	Corynebacterium g1
122	7	1.4	397	20	AAU35476	Chlamydia pneumonia
123	7	1.4	399	22	AAU71595	Arabidopsis thalia
124	7	1.4	402	21	AAU54363	Arabidopsis thalia
125	7	1.4	402	22	AAU20527	Human secreted pro
126	7	1.4	406	22	ABG11445	Novel human diago
127	7	1.4	408	20	AAU41111	Human TANGO 129 (T
128	7	1.4	414	22	AAU32999	Novel human secret
129	7	1.4	418	22	AAU91830	C glutamicum prote
130	7	1.4	429	22	ABG09437	Human TGF-beta rec
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132	7	1.4	430	21	AAU41110	Human tumour necro
133	7	1.4	430	21	AAU70785	Human tumour necro
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142	7	1.4	466	20	AAU50341	Human K6.2 protei
143	7	1.4	466	22	ABG11444	Novel human diago
144	7	1.4	481	19	AAU83216	Human h-RAB-R... HO
145	7	1.4	481	19	AAU50342	Human K6.2 prote
146	7	1.4	481	22	AAU04758	Human vesicle traf
147	7	1.4	502	22	ABU69102	Drosophila melanog
148	7	1.4	510	22	AAU84250	Amino acid sequenc
149	7	1.4	522	22	AAU84250	R. marinus bacteri
150	7	1.4	526	21	AAU54362	Arabidopsis thalia

ALIGNMENTS

ID	AAU13360 standard; Protein: 490 AA.
XX	AAU13360;
AC	25-JUN-1999 (first entry)
XX	Amino acid sequence of protein PRO269.
DE	Secreted protein; transmembrane protein; human; enterocolitis;
XX	Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW	congenital microvillus atrophy; skin disease; cell growth;
KW	abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW	Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
KW	fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
KW	anti-thrombotic; wound healing; tissue repair.
OS	Homo sapiens.
XX	WO914328-A2.
PD	25-MAR-1999.
XX	16-SEP-1998; 98WO-US19330.
PF	25-NOV-1997; 97US-0066840.
PR	17-SEP-1997; 97US-0059113.
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PR 24-NOV-1997; 97US-0066453.
XX (GETH ) GENENTECH INC.
XX Chen J, Goddard A, Gurney AL, Pennica D, Wood WL, Yuan J;
XX WPI: 1999-229533/19.
XX N-PSDB; AAX52231.
XX
XX New isolated human genes and polypeptides used in, e.g. treatment of
XX gastrointestinal ulceration
XX
XX Claim 12; Fig 36; 320pp; English.
XX
XX AAV1344-403 represent secreted and transmembrane human proteins.
XX The cDNA sequences are obtained from cDNA libraries, prepared from
XX fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
XX The encoded polypeptides have specific uses based on their homology to
XX known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
XX associated with the preservation and maintenance of gastrointestinal
XX mucosa and the repair of acute and chronic mucosal lesions
XX (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
XX ulceration and congenital microvillus atrophy), skin diseases associated
XX with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
XX cancers such as lung squamous cell carcinoma of the vulva and gliomas),
XX potent effects on cell growth and development, diseases related to
XX growth or survival of nerve cells including Parkinson's disease,
XX Alzheimer's disease, AIDS, neuropathies or cancer. PRO265 can be used as
XX for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
XX as a target for anti-tumor drugs. PRO533 may be used in the treatment
XX of Usher Syndrome or Atrophia areata. PRO269 can be used as an
XX anti-thrombotic agent; PRO287 polypeptides and portions may have
XX therapeutic applications in wound healing and tissue repair; PRO317 can
XX be used for treating problems of the kidney, uterus, endometrium, blood
XX vessels, or related tissue, e.g. in the heart of genital tract.
XX
XX Sequence 490 AA:
XX
XX Query Match 100.0%; Score 490; DB 20; Length 490;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 421 vlcifhespspprkessmpgldespepaalgssahctmgvkvgdcdlrdregall 480
OY 481 AESPLGSSDA 490
DB 481 aesplgssda 490
XX
XX RESULT 2
XX AAB33460
XX ID AAB33460 standard; Protein; 490 AA.
XX
XX AAB33460;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human PRO269 protein UNQ236 SEQ ID NO:233.
XX
XX Human; immune related disease; diagnosis; antiinflammatory; cardiact;
XX dermatological; antlathritic; antlthneumatic; immunosuppressive;
XX haemostatic; antlthyroid; antidiabetic; nootropic; neuroprotective;
XX antlanemic; hepatotropic; virucide; antiporiatic; antiallergic;
XX antlathmatic; systemic lupus erythematosus; rheumatoid arthritis;
XX osteoarthritis; spondylarthropathy; systemic sclerosis; sarcoidosis;
XX idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
XX systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
XX autoimmune thrombocytopenia; immune-mediated renal disease;
XX demyelinating disease; hepatobiliary disease; Whipple's disease;
XX inflammatory bowel disease; gluten-sensitive enteropathy;
XX autoimmune disease; immune-mediated skin disease; allergic disease;
XX immunological disease; transplantation associated disease;
XX graft rejection; graft-versus-host-disease.
XX
XX Homo sapiens.
XX
XX WO200053758-A2.
XX
XX 14-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US05841.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 10-MAR-1999; 99US-0123618.
XX 12-MAR-1999; 99US-0123957.
XX 23-MAR-1999; 99US-0123775.
XX 12-APR-1999; 99US-0128849.
XX 20-APR-1999; 99WO-US08615.
XX 28-APR-1999; 99US-0131445.
XX 04-MAY-1999; 99US-0132371.
XX 14-MAY-1999; 99US-0134287.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX 28-JUL-1999; 99US-0146222.
XX 01-SEP-1999; 99WO-US20111.
XX 08-SEP-1999; 99WO-US20594.
XX 13-SEP-1999; 99WO-US20944.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 29-OCT-1999; 99US-0162506.
XX 29-NOV-1999; 99WO-US28214.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30999.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.

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06-JAN-2000; 2000MO-US00277
 06-JAN-2000; 2000MO-US00376
 11-FEB-2000; 2000MO-US03565
 18-FEB-2000; 2000MO-US04341
 18-FEB-2000; 2000MO-US04342
 22-FEB-2000; 2000MO-US04414

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W,
 PI Kabakoff RC, Lu Y, Pan Y, Pennica D, Shelton DJ, Smith V,
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 DR WPI; 2000-572271/53.
 DR N-PSDB: AAC58625.

PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

XX Claim 33; Fig 94; 309pp; English.

CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathes,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, guttate sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC diseases including diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 CC AAC33414 to AAC33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.

XX Sequence 490 AA;

Query Match 100.0%; Score 490; DB 21; Length 490;

Best Local Similarity 100.0%; P-vec No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRPAFALCLIMQALWPGGSGEHPTRDRACCSAGACYSLHATMKROAAEEACILRGCA 60
 1 mrpafalclimqalwpggsggehpdracccsagacyslhahmtkrroaaeeacilrgca 60
 61 LSTVRAGAEELRAVLALLRGGPGGSKDLFFVALERRRSNCTLENEPLRGFSWISDP 120
 61 lstrvragaelravalllrrggpggskdlffvalerrrsnctleneplrgfswisddp 120
 121 GGLSEDTLQWVEPORSCTARRCAVLQATGVEPAGMKEMRCHLRANGVLCYQOEVLCP 180
 121 gglseDTLQWVEPORSCTARRCAVLQATGVEPAGMKEMRCHLRANGVLCYQOEVLCP 180
 121 gglseDTLQWVEPORSCTARRCAVLQATGVEPAGMKEMRCHLRANGVLCYQOEVLCP 180
 181 APPRGASNSRYAPRQSLAALDSFPTREVSALCRGOLPSVTCTIAETIGARDKLSG 240
 181 apprgasnsryaprqslaaldsfptrevsalcrqolpsvtctiaetigarDKLSG 240
 181 apprgasnsryaprqslaaldsfptrevsalcrqolpsvtctiaetigarDKLSG 240
 241 DVLCPCGRYLRAGKCAELPNCIDLDGFGACATGFEIGKRGRCVNSGEOPPLGSG 300
 241 dvlcpcgrylragkcaelpncidldgfgacatgfeigkrgrcvnsgeopplgsg 300
 241 dvlcpcgrylragkcaelpncidldgfgacatgfeigkrgrcvnsgeopplgsg 300
 301 VPLTRPATATSPVQRTWPIVDEKLGETPLVPEODMSVTSIPEIPWGSOSTWSTLQ 360
 301 vpltrpatatSPVQRTWPIVDEKLGETPLVPEODMSVTSIPEIPWGSOSTWSTLQ 360
 301 vpltrpatatSPVQRTWPIVDEKLGETPLVPEODMSVTSIPEIPWGSOSTWSTLQ 360

OY 361 SLQAEKATINPSSGVSISKFNSTSSATPQAFDSSAVFEIPEVSTAVVLVILTMVVLGL 420
 Db 361 slqaeKATINPSSGVSISKFNSTSSATPQAFDSSAVFEIPEVSTAVVLVILTMVVLGL 420
 OY 421 VKLCFHESPSQPRKESMGPGLESDPEPALGSSSAHCTNNCKVKGDCOLRRRAGALL 480
 Db 421 vklcfhESPSQPRKESMGPGLESDPEPALGSSSAHCTNNCKVKGDCOLRRRAGALL 480
 OY 481 AESPLGSSDA 490
 Db 481 aesplgssda 490

RESULT 3
 AAB24403
 ID AAB24403 standard; Protein: 490 AA.
 AC AAB24403;
 XX 07-NOV-2000 (first entry)

DE Human PRO269 protein sequence SEQ ID NO:77.

KW Human: PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiac; cardiovascular; antithrombotic;
 KW cytosolic; gene therapy; vaccine.

OS Homo sapiens.

PN WO200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1998; 98WO-US25108.

XX 16-DEC-1998; 98US-0112850.

XX 12-JAN-1999; 99US-0115554.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145608.

XX 01-SEP-1999; 99WO-US20111.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 05-SEP-1999; 99WO-US21547.

XX 29-OCT-1999; 99WO-US23089.

XX 29-OCT-1999; 99US-0162506.

PA (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A,
 XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V,
 XX Watanabe CK, Williams PM, Wood WI;
 DR WPI; 2000-412154/35.
 DR N-PSDB: AAA77570.

PT Nucleic acids encoding PRO polypeptides useful for preventing,
 PT diagnosing and treating disorders in mammals
 PT angiogenic disorders in mammals

PS Claim 72; Fig 32; 315pp; English.

CC The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating disorders in mammals by
 CC cardiovascular, endothelial or angiogenic disorder in mammals by

modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The CC nucleic acids and the proteins they encode may be used in the CC prevention, treatment and diagnosis of diseases associated with CC. Inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AA77510 to AA77721 and CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.

Sequence 490 AA:

Query Match 100.0%; Score 490; DB 21; Length 490;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRPAFLCLLMQALMPGCGEHPTADRAAGCSAGACYSLHNTMKROAAEACILRGGA 60
1 mrfafclllwqalwpgpggghptadragcsasagacyslhntmrqaaeeacilrgga 60
61 LSTVRAGAEIRAVLALLRAGPGGSGKDLLFWALERRSHCTLENEPLRGFSWLSPP 120
61 lstrvragaelravalllrpgpggsgskdllfwalerrshctleneplrgfswlsdp 120
121 GLESDTLQWVEEPPORSCSTARCAVLAQATGVEPAGKEMRCHLRANGYLCKYQFEVLCP 180
121 glesdtlqweepqscstarccavlaqatgvepaggkwmrchlrrangylckyqfevlcp 180
181 APRGAASNLSTRAPQLHSAALDFSPPTGVSAICRGQLPISVTCIADIGARMWKLGG 240
181 aprgaasnlsyrapqlhsaaldfspptgvsaicrgqlpistctiadegarmwklsg 240
241 DVLCPGPGYRLAAGKCAEPLNCLDGLGAGCAATGFEIGKORSCVTSGEQPTIGGG 300
241 dvlcppgpyrlagkcaelpncldlglgagcaatgfeigkgrscvtsgeqptlggg 300
301 VPTRRPATATSPVQRTWPIRVDKLGETPLVPEODNSVTSIPEIPRMGSOSTMSTLQM 360
301 vptrrpatatspvqrtwpirvdkgetplvpeodnsvtsipeiprmgsostmstlqm 360
361 SIQAEKATITSGSVISKFNSTSSATQAPDFSSAVVFIPSTAVVILITMVLGL 420
361 siqaekatitpsgviskfnstssatqapdfssavvfipstavvilltmvlgl 420
421 VILCFHESPSQPRKESMPGGLSEDPPEPALGSSSAHCTNNGVKYGDDCLDRAGCALL 480
421 vilcfhespsqprkesmpgglsedeppepalgssahctnnkvkygddclldragcall 480
481 AESPLGSSDA 490
481 aesplgssda 490

DB 481 aesplgssda 490

RESULT 4
AA95016
ID AA95016 standard; Protein; 490 AA.

AC AA95016;

DT 19-JUN-2000 (first entry)

DE Human secreted protein vp15_1, SEQ ID NO:72.

XX Human: secreted protein; cancer: tumour; cardiovascular disorder:

KM blood disorder: haemophilia; autoimmune disease: diabetes; inflammation:

KM infection: fungal; bacterial; viral; HIV; allergy; arthritis;

XX neurodegenerative disease: asthma; contraceptive.

OS Homo sapiens.

PN WO200011015-A1.
XX 02-MAR-2000.
XX 24-AUG-1999; 99WO-US19351.
PR 24-AUG-1998; 98US-0097638.
PR 24-AUG-1998; 98US-0097659.
PR 09-SEP-1998; 98US-0099618.
PR 28-SEP-1998; 98US-0102092.
PR 25-NOV-1998; 98US-0109978.
PR 23-DEC-1998; 98US-0113645.
PR 23-DEC-1998; 98US-0113646.
PR 23-AUG-1999; 99US-0379246.
XX (ALPH-) ALPHAGENE INC.
XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
PI WPI; 2000-224657/19.
XX New secreted or transmembrane proteins and polynucleotides encoding
PT them, useful for treating neurodegenerative disorders, autoimmune
PT diseases and cancer -
XX Claim 81: Page 331-332; 357pp; English.
XX The invention relates to 40 human secreted proteins (AA94981-Y95020),
XX and CDNA sequences encoding them (AA23423-A23462). The secreted
XX proteins of the invention include those that are thought to be only
XX partially secreted, i.e., transmembrane proteins. The proteins of the
XX invention may exhibit one or more activities selected from the following:
XX cytokine activity; cell proliferation; differentiation; immune
XX modulation; haematopoiesis regulation; tissue growth activity;
XX activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
XX and thrombolytic activity; anti-inflammatory activity; and tumour
XX inhibition activity. The proteins may be administered to patients as
XX vaccines, and the nucleotides may be used as part of a gene therapy
XX regime. Diseases or conditions that may be treated using the proteins or
XX nucleotides of the invention include autoimmune diseases; genetic
XX disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
XX fungal and viral infections, especially HIV; multiple sclerosis;
XX rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
XX insulin dependent diabetes mellitus; and allergic reactions such as
XX asthma and anaemia. They may also be used for treating wounds, burns,
XX ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
XX disease, Parkinson's disease, Huntington's disease and amyotrophic
XX lateral sclerosis (ALS). Proteins with activin/inhibin activity may
XX additionally be useful as contraceptives. Nucleic acid sequences of the
XX invention may be used in chromosome mapping, and as a source of
XX diagnostic primers and probes. The present sequence represents one of the
XX 40 proteins of the invention.

Sequence 490 AA:

Query Match 100.0%; Score 490; DB 21; Length 490;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRPAFLCLLMQALMPGCGEHPTADRAAGCSAGACYSLHNTMKROAAEACILRGGA 60
1 mrfafclllwqalwpgpggghptadragcsasagacyslhntmrqaaeeacilrgga 60
61 LSTVRAGAEIRAVLALLRAGPGGSGKDLLFWALERRSHCTLENEPLRGFSWLSPP 120
61 lstrvragaelravalllrpgpggsgskdllfwalerrshctleneplrgfswlsdp 120
121 GLESDTLQWVEEPPORSCSTARCAVLAQATGVEPAGKEMRCHLRANGYLCKYQFEVLCP 180
121 glesdtlqweepqscstarccavlaqatgvepaggkwmrchlrrangylckyqfevlcp 180
181 APRGAASNLSTRAPQLHSAALDFSPPTGVSAICRGQLPISVTCIADIGARMWKLGG 240

PN	MO2001.040466-A2.
PP	
PD	07-JUN-2001.
XX	
PF	01-DEC-2000; 2000MO-US32678.
XX	
01-DEC-1999;	99MO-US28301.
01-DEC-1999;	99MO-US28634.
02-DEC-1999;	99MO-US28531.
02-DEC-1999;	99MO-US28564.
02-DEC-1999;	99MO-US28565.
09-DEC-1999;	99US-0170262.
16-DEC-1999;	99MO-US30095.
20-DEC-1999;	99MO-US30911.
20-DEC-1999;	99MO-US30999.
30-DEC-1999;	99MO-US31243.
06-JAN-2000;	2000MO-US00277.
06-JAN-2000;	2000MO-US00376.
11-FEB-2000;	2000MO-US03565.
18-FEB-2000;	2000MO-US04341.
18-FEB-2000;	2000MO-US04342.
22-FEB-2000;	2000MO-US04914.
24-FEB-2000;	2000MO-US04914.
01-MAR-2000;	2000MO-US05004.
01-MAR-2000;	2000MO-US05004.
21-MAR-2000;	2000MO-US07377.
21-MAR-2000;	2000MO-US07532.
30-MAR-2000;	2000MO-US08438.
17-MAY-2000;	2000MO-US13705.
23-MAY-2000;	2000MO-US14042.
30-MAY-2000;	2000MO-US14941.
02-JUN-2000;	2000MO-US15264.

	Query Match	Similarity	100.0%	Score 490;	DB 22;	Length 490;
	Best Local	Similarity	100.0%	Pred. No. 0;		
	Matches 490;	Conservative	0;	Mismatches	0;	Indels
						Gaps
QY	1	MRPAFLCLIMQALIMPQGGGEHPTADRGCSGAGCYLSLHATFMKROAAEFACILRGGA	60			
DB	1	mrpafalcilwqalwlpqpggghptadrgccassgagcyslhhatmrrgaeeacilrrga	60			
QY	61	LSYVRGAELRAVLALLRRGPGGGGSKDILFWALERRRSHCTLENEPLRGFSWISDP	120			
DB	61	lsctvragaelrravalllrrgpgpgyskalllwalertrrrhctlenepilrgfswisdp	120			
QY	121	GGLESDDLQWVEEPPQRSCFARRCAYLQAGGVEPAGWKMRCMHLRANGLCYKYOEPHYCP	180			
DB	121	gglesdltlqweeppqrscfarrcavilqatggyepagwkmrchllranylrcykgyevlcp	180			
QY	181	ARRPQAASNLSTRAPQQLHSAALDSSPECTEXSALCRGOLPTSVTICITADEIGARDKLSG	240			
DB	181	arrpqaasnlstrapfqhsaalidsppletevalorgllpivsticidaeigarwdklsg	240			
QY	241	DVLCPGPGRYLAGACAEELPNCIDLDGACACCAAGFELGKRGRSCVYNSGEQPLRGSGT	300			
DB	241	dvlcpogpryilagcaelpncldldgacaccaagfelgkrgkrscvysgeeqplrgsgt	300			
QY	301	VTRRPPEATATSPVQRTWPIRIVDEKLGETPLVLPBDNSVTSIPEIPWGSOSTSTROM	360			
DB	301	vtrrppeatatsvprqtwplirvdekigetplvpeqdnsvtsipeipwqsgstmsltqm	360			
QY	361	SLQASKATITPGSGVIEKFNSTSSATPOAFOSSSAVFLFEVSRNAVVLVILMTFVGL	420			
DB	361	slqaskatitpgsgviskfntslssatpqaafssavvlfevsvrnavvlvilmfvtgl	420			

OY 421 VKLCHESSOPRKESMPGLESDPEPALGSSSAHCTNNGVGVCDLDRAGALL 480
 DB 421 VKLCHESSOPRKESMPGLESDPEPALGSSSAHCTNNGVGVCDLDRAGALL 480
 OY 481 AESPLGSSDA 490
 DB 481 aesplgssda 490
 RESULT 6
 AAE06596
 ID AAE06596 standard; Protein: 490 AA.
 AC AAE06596;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Human protein having hydrophobic domain, HP03983.
 XX
 KW human; hydrophobic domain; gene therapy; nutritional supplement;
 KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
 KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
 KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
 KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
 KW contraceptive; antiinfectivity; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= Signal_peptide
 FT 23..490
 FT /note= "Mature human protein with hydrophobic domain"
 XX
 PN WO200149728-A2.
 PD 12-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-JP09359.
 XX
 PR 06-JAN-2000; 2000JP-0000585.
 PR 06-JAN-2000; 2000JP-0000588.
 PR 11-JAN-2000; 2000JP-0002239.
 PR 03-FEB-2000; 2000JP-0026862.
 PR 03-MAR-2000; 2000JP-0058367.
 XX
 PA (PROT-) PROTEGENE INC.
 PA SAGA) SAGAMI CHEM RES CENT.
 XX
 PI Kato S, Kimura T;
 XX
 DR WPI: 2001-418355/44.
 DR N-PSDB: AAD12591.
 XX
 PT Human proteins with hydrophobic domains and the nucleic acids encoding
 PT them, useful for preventing diagnosing and treating e.g. cancer,
 PT Alzheimer's and inflammation
 XX
 PS Claim 1; Page 110-111; 563pp; English.
 XX
 CC The present sequence is human protein with hydrophobic domain,
 CC HP03983. The polynucleotide and polypeptide of the invention
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The polynucleotides
 CC may be used to produce the polypeptide, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. The
 CC polynucleotide and its complementary sequences may also be used as DNA
 CC probes in diagnostic assays and also used in gene therapy. The
 CC polypeptides may also be used as antigens in the production of antibodies
 CC and in assays to identify modulators of polypeptide expression and
 CC activity. The polypeptides and nucleic acids may be used as nutritional

CC supplements, to modulate cytokine and cell proliferation activity, to
 CC modulate immune stimulation or suppression (e.g. for the treatment of
 CC microbial infections and autoimmune disorders such as multiple sclerosis,
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
 CC disease), to modulate activin and inhibin activity (e.g. for controlling
 CC fertility), to modulate chemotactic and chemokinetic activity, to
 CC modulate haemostatic and thrombolytic activity, to modulate receptor
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.
 XX
 SO Sequence 490 AA:
 Query Match 100.0%; Score 490; DB 22; Length 490;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MRPAFLCLWQALMPGGGHEPTADRAGSAGSAGSGLHATMKROAEACILRGCA 60
 DB 1 mpaflcllwqalwpgpggheptadragcsagacsylhatamkrgaaeacillrga 60
 OY 61 ISTVAGAEIRAVLALLRAGPGGGSKDLFWVALERRSHCTLENPLRFSMLSDP 120
 DB 61 istvagaelravlaallragpgggskdlfwvalerrshctleneplyrfsmlsdp 120
 OY 121 GLESDTLQWVEEPORSCSTARCAVLQATGVEPAGWKEMRCHLRANGYLCKYQFEVLCP 180
 DB 121 glesdttlqwveeporscstarcaavlqatgvepagwkemrchlranlylckyqfevlcp 180
 OY 181 APRPAASNLSTRAPOLHSAALDFSPCTEVSALCRGLPISTVCIADETARMDKLSG 240
 DB 181 aprpaasnlsyrapqlhsaaldfspctevsalcrglplstvciaadelgarvdklsg 240
 OY 241 DVLCPGGRYLKAGCAELPNCIDLDGFCACATGEFLGKRGSCVSGEOPITLGNG 300
 DB 241 dvlcpgrlylragkcaelpncidldgfcacatgelfgkrgscvsggeopitlgng 300
 OY 301 VPTRRPATATSPVQRTWPRIWDEKLGFTPLVPBDNSVTSIPEIPRMKSQSTNTSLQW 360
 DB 301 vptrrpatatpvpqrtpwprirwdeklgftplvpbdnsvtsipeiprmksqstntslqw 360
 OY 361 SIQASKATITPSSGVISFNFTSSATPOADSSAVETIVSTRVAVILMTVTGL 420
 DB 361 siqaeskatitpssgvvisfnftssatpoadssavetivstravavilmtvtgl 420
 OY 421 VKLCHESSOPRKESMPGLESDPEPALGSSSAHCTNNGVGVCDLDRAGALL 480
 DB 421 VKLCHESSOPRKESMPGLESDPEPALGSSSAHCTNNGVGVCDLDRAGALL 480
 OY 481 AESPLGSSDA 490
 DB 481 aesplgssda 490
 RESULT 7
 AAB41847
 ID AAB41847 standard; Protein: 331 AA.
 AC AAB41847;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORF1611 polypeptide sequence SEQ ID NO:3222.
 XX
 KW Human; open reading frame; ORF; detection; cytostatic; hepatotropic;
 KW vlnetary; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antiidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antineumatic; antihypertoid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;

KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.
 OS Homo sapiens.
 JN WO200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000. 2000MO-US08621.
 XX
 PR 31-MAR-1999. 99US-0127607.
 PR 02-APR-1999. 99US-0127636.
 PR 05-APR-1999. 99US-0127728.
 PR 30-MAR-2000. 2000US-0540763.
 (CURA-) CUBAGEN CORP.
 XX
 PI Shinkels RA, Leach M;
 DR WPI: 2000-602362/57.
 DR N-PSDB: AAC76056.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 PS Claim 11; Page 2431-2432; 5507pp; English.
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antiproliferative; antiparkinsonian; neurotropic; neuroprotective;
 CC osteoplastic; anticonvulsant; antidiabetic; immunosuppressive;
 CC antidiabetic; hypoglycemic; thrombolytic; coagulant; vasotropic;
 CC antihypertensive; antihypertensive; antiviral; antifungal; antineoplastic;
 CC antihypertensive; antihypertensive; antihypertensive; antihypertensive;
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy.
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 SO Sequence 331 AA.
 Query Match 60.4%; Score 296; DB 21; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1.4e-284;
 Matches 296; Conservative 0; Mismatches 0; Indels 10; Gaps 0;
 OY 147 OATGVEPAGKEMRCHIRANGYLCCKYQFVLCAPRGAASNLSTYAPFOLHSALDFS 206
 DB 33 gdtgvepawgkwmchlrangylckqfeylcpaprgaasnlstypafqlhsaalfs 92
 OY 207 PGTVEVALCRGQLPSTVTCIADFGARMDLSDVLCPCGRTLRGKCAELPNCIDL 266
 DB 93 pgtvvalcrgqlpstvctiadefgarwdlsgdvclpcpgrtlyrkgkaelpnciddl 152
 OY 267 GGFACGATGELGKGRSCVTSSEGOPTLGGTCVPTRRPAPATSPVPORTMPTIVDEK 326
 DB 153 ggfaccgatgelgkgrscvtsssegoptlggtcvptrrpapatspvportmptivdek 212

OY 327 IGFETPIVPEQDNSTSTIPETPRWGSQSTMTLOMSLOAESKATITPSSGVISKFNSTSS 386
 DB 213 lgefpivpeqdnststipetprwgsqstmtlomsloaeskatitpssgviskfnstss 272
 OY 387 ATPQAFDSSSAVVFVSTAVVAVITMTVGLVYVLCFHESSSQPRRESKCPG 442
 DB 273 atpafidsssavvfivstavvavitmtvlglyvlycchesssqprreskcpmgpg 328
 RESULT 8
 AA91410
 ID AAY91410 standard; Protein; 344 AA.
 XX
 AC AAY91410;
 XX
 DT 29-JUN-2000 (first entry)
 XX
 DE Human secreted protein sequence encoded by gene 4 SEQ ID NO:131.
 KW Human; secreted protein; diagnosis; neuroprotective; neurotropic;
 KW neuroleptic; antianemic; cerebroprotective; immunomodulatory;
 KW anti-microbial; cardiac; cytostatic; antiinflammatory; haemostatic;
 KW anticonvulsant; vasotropic; vaccine; gene therapy; anti-sense therapy;
 KW neutral; reproductive; immune disorder; immunodeficiency; infection;
 KW lymphoma; demyelinating disease; autoimmune; cancer; inflammation;
 KW aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; Tourette syndrome; multiple sclerosis; meningitis;
 KW ischaemia; mania; dementia; obsessive compulsive disorder; sexually-linked disorder;
 KW viral prophylaxis; developmental disorder; food additive; preservative; chromosome 14.
 XX
 OS Homo sapiens.
 XX
 JN WO200011014-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 24-AUG-1999. 99WO-US19330.
 XX
 PR 25-AUG-1998. 98US-0097917.
 PR 31-AUG-1998. 98US-0098634.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Moore PA, Ruben SM, Olsen HS, Shi Y, Rosen CA, Florence KA,
 PI Soppet DR, Lafleur DW, Endress CA, Ebner R, Komatsoulis G;
 PI Duan RD;
 DR WPI: 2000-224656/19.
 XX
 PT Novel secreted proteins and corresponding DNA molecules that can be
 PT used to prevent, treat and diagnose disease in humans, for example,
 PT Alzheimer's, cancer, and immune disorders -
 XX
 PS Disclosure; Page 391-392; 416pp; English.
 XX
 The polynucleotide sequences given in AAA26281 to AAA26336 encode the
 CC human secreted proteins given in AAY91346 to AAY91449. The human secreted
 CC proteins can have activities based on the tissues and cells they are
 CC expressed in. Examples of the activities are: neuroprotective; neurotropic;
 CC neuroleptic; antianemic; cerebroprotective; immunomodulatory;
 CC anti-microbial; cardiac; cytostatic; antiinflammatory; haemostatic;
 CC anticonvulsant; and vasotropic. The polynucleotides and proteins may be
 CC used to prevent, treat or ameliorate a medical condition, e.g. by protein
 CC or gene therapy. Conditions treatable by the proteins of the invention
 CC include neural, reproductive, or immune disorders, especially
 CC immunodeficiency, infection, lymphomas, demyelinating diseases,
 CC auto-immunities, cancer, general microbial infection, inflammation,
 CC aneurysms and haemorrhages. Specific examples include: Alzheimer's
 CC disease; Parkinson's; Huntington's; Tourette syndrome; multiple
 CC sclerosis; meningitis; ischaemia; prostate cancer; mania; dementia;
 CC obsessive compulsive disorder and viral prophylaxis. The polynucleotides

and proteins can also be used in the detection of disorders associated with the function of the protein, for example, the detection of developmental disorders, sexually-linked disorders, or disorders of the cardiovascular system. They may also be used as food additives or preservatives. AAA26272 to AAA26280 and AAY91345 are sequences used in the exemplification of the present invention.

Sequence 344 AA:

Query Match 55.9%; Score 274; DB 21; Length 344;
Best Local Similarity 100.0%; Pred. No. 9.4e-263;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

169 YLCKYQFVLCPPAPGASNLSTYRAPQLHSAALDFSPGTEVSALRGQLPISVTCTA 228
23 YLCKYQFVLCPPAPGASNLSTYRAPQLHSAALDFSPGTEVSALRGQLPISVTCTA 82
229 DEIGARMKLSGDVLCPCPGRIKLRGKCAELPNCDDLGCFACGATGFEKDGRCVY 288
83 delgerwklsgdvlicpcpgrylrqkcaelpncddlgfcecaltgfejqkdgrrscvt 142
289 SGEQPTLGTGCVPRRPATSPVPORTWPIRVDKLGEPPLVEODNSTVSIPEIPR 348
143 sgegptlgtgcvprrrpatatpvtprtwpirvdekigtetplvpeqdnsvtsipeipr 202
349 WGSOSTMSTLQMSLOAESKATIPSGSVISKFNSTSSATPOAFDSSSAVVEIFVSTAV 408
203 wsgostmstlqmsloaeskatipsgsviskfnstssatpofadssavvelfvstlav 262
409 VLVITMTVLGIVKICFHSPPSSOPRKESMPG 442
263 vlvitmtvlgivkicfhspssoprkessmpg 296

RESULT 9

AAB80228
ID AAB80228 standard; Protein: 428 AA.

AC AAB80228;

DT 24-APR-2001 (first entry)

DE Human PRO269 protein.

XX Human; PRO: dermatological; antipsoriatic; cytostatic; antinflammatory;

KW antiParkinsonian neurologic; neuroprotective; vulnerrary; cardiac;

KW antiangiogenic; vasotropic; antihistaminic; antirheumatic; cancer;

KW antiarthritic; antiinfectility; antidiabetic; antiviral; diabetes;

KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;

KW schaeemia; inflammation.

XX Homo sapiens.

OS WO200104311-A1.

PD 18-JAN-2001.

PE 22-FEB-2000; 2000WO-US04414.

XX 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145638.
XX 28-JUL-1999; 99US-0146222.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.

PR 05-JAN-2000; 99WO-US00219.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavlin IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WI;

DR WPI: 2001-081051/09.

DR N-PSDB: AAF72289.

PT Sixty one nucleic acids encoding PRO polypeptides which are useful in

PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung

PT squamous cell carcinoma) and neurodegenerative diseases (e.g.

PT Alzheimer's disease)

XX Claim 1: Fig 36; 393bp; English.

PS The present sequence is one of sixty one novel secreted and

CC transmembrane PRO polypeptides. The PRO polypeptides are

CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung

CC squamous cell carcinoma), gastrointestinal disorders (e.g. lung

CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,

CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.

CC endometrial bleeding angiogenesis, ischaemias such as coronary

CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,

CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and

CC diabetes and retinal disorders such as retinitis pigmentosa.

CC The PRO nucleic acids have applications in molecular biology, including

CC use as hybridization probes, and in chromosome and gene mapping.

XX Sequence 428 AA:

Query Match 49.4%; Score 242; DB 22; Length 428;
Best Local Similarity 100.0%; Pred. No. 5.6e-231;

Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 RYLKAGKCAELPNCDDLGCFACGATGFEKDGRCVTSGEQPTLGTGVPTRRPPA 308

DB 187 YLIRAGKCAELPNCDDLGCFACGATGFEKDGRCVTSGEQPTLGTGVPTRRPPA 246

QY 309 TATSPVORTWPIRVDKLGEPPLVEODNSTVSIPEIPRMGSOSTMSTLQMSLOAESKA 368

DB 247 latspvprtwpirvdekigtetplvpeqdnsvtsipeiprwsgstmslqmsloaeska 306

QY 369 TTTPSGSVISKFNSTSSATPOAFDSSSAVVEIFVSTAVVILMTVLGIVKICFHS 428

DB 307 tltpsgsviskfnstssatpofadssavvelfvstlavviltvlgivkicfhhs 366

QY 429 PSSOPRKESMPGPLESDEPAALGSSAHNCTNCKVGDGDLRDRAGALIAESPLSS 488

DB 367 pssoprkessmpgplesepeaalgssahncnkvvgdcdlrdraegaaliaesplss 426

QY 489 DA 490

DB 427 da 428

XX 19-JUN-2000 (first entry)

XX Human clone vpl5.1 insertional variant ORF, SEQ ID NO:131.

XX Human; secreted protein; cancer; tumour; cardiovascular disorder;

KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;

RESULT 10

AAV95031
ID AAV95031 standard; Protein: 175 AA.

AC AAV95031;

DT 19-JUN-2000 (first entry)

DE Human clone vpl5.1 insertional variant ORF, SEQ ID NO:131.

XX Human; secreted protein; cancer; tumour; cardiovascular disorder;

KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;

KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
 KW neurodegenerative disease; asthma; contraceptive; open reading frame;
 KW ORF; variant.

OS Homo sapiens.

XX WO200011015-A1.

XX 02-MAR-2000.

XX 24-AUG-1999; 99WO-US19351.

XX 24-AUG-1998; 98US-0097638.

XX 24-AUG-1998; 98US-0097659.

XX 09-SEP-1998; 98US-0099618.

XX 28-SEP-1998; 98US-0102092.

XX 25-NOV-1998; 98US-0109978.

XX 23-DEC-1998; 98US-0113645.

XX 23-DEC-1998; 98US-0113646.

XX 23-AUG-1999; 99US-0379246.

XX (ALPH-) ALPHAGEN INC.

XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapieko P.

XX WPI: 2000-224657/19.

XX New secreted or transmembrane proteins and polynucleotides encoding

XX them, useful for treating neurodegenerative disorders, autoimmune

XX diseases and cancer -

XX Disclosure: Page 351; 357pp; English.

XX The invention relates to 40 human secreted proteins (AAV94981-Y95020),

XX and cDNA sequences encoding them (AA23423-A23462). The secreted

XX proteins of the invention include those that are thought to be only

XX partially secreted, i.e., transmembrane proteins. The proteins of the

XX invention may exhibit one or more activities selected from the following:

XX cytokine activity; cell proliferation; differentiation; immune

XX modulation; haematopoiesis regulation; tissue growth activity;

XX activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic

XX and thrombolytic activity; anti-inflammatory activity; and tumour

XX inhibition activity. The proteins may be administered to patients as

XX vaccines, and the nucleotides may be used as part of a gene therapy

XX regime. Diseases or conditions that may be treated using the proteins or

XX nucleotides of the invention include autoimmune diseases; genetic

XX disorders; haemophilia; cardiovascular diseases; cancer; bacterial,

XX fungal and viral infections, especially HIV; multiple sclerosis;

XX rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;

XX insulin dependent diabetes mellitus; and allergic reactions such as

XX ulcers, osteoporosis, osteoarthritis, periodontal diseases, burns,

XX disease, Parkinson's disease, Huntington's disease and amyotrophic

XX lateral sclerosis (ALS). Proteins with activin/inhibin activity may

XX additionally be useful as contraceptives. Nucleic acid sequences of the

XX invention may be used in chromosome mapping, and as a source of the

XX CC diagnostic primers and probes. Sequences AAV95024-Y95025, AAV95029 and

XX CC AAV95031-Y95032 represent additional open reading frames (ORFs) that are

XX CC encoded by deletion or insertional variants of the cDNA clones of the

XX CC invention.

XX Sequence 175 AA:

XX

XX

XX

XX

DB 61 1stviragaelravallalragp99gskdl1fwalerrshc1lenep1rgfswlssdp 120

OY 121 GGLSDPTQWWEFQRCST 139

DB 121 99lesd1qvwepqrst 139

RESULT 11

AAV91349

ID AAV91349 standard; Protein; 189 AA.

XX AAV91349;

XX 29-JUN-2000 (first entry)

DE Human secreted protein sequence encoded by gene 4 SEQ ID NO:70.

XX Human: secreted protein; diagnosis; neuroprotective; nootropic;

XX neuroleptic; anti-manic; cerebroprotective; immunomodulatory;

XX anti-microbial; cardiac; cytosolic; anti-inflammatory; haemostatic;

XX anticoagulant; vasotropic; vaccine; gene therapy; anti-sense therapy;

XX neural; reproductive; immune disorder; immunodeficiency; infection;

XX lymphoma; demyelinating disease; autoimmunity; cancer; inflammation;

XX aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disease;

XX Huntington's disease; Tourette syndrome; multiple sclerosis; meningitis;

XX ischaemia; mania; dementia; obsessive compulsive disorder;

XX viral prophylaxis; developmental disorder; sexually-linked disorder;

XX cardiovascular disorder; food additive; preservative; chromosome 14.

OS Homo sapiens.

XX WO200011014-A1.

XX 02-MAR-2000.

XX 24-AUG-1999; 99WO-US19330.

XX 25-AUG-1998; 98US-0097917.

XX 31-AUG-1998; 98US-0098634.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Moore PA, Ruben SM, Olsen HS, Shi Y, Rosen CA, Florence KA;

XX Soppet DR, Lafleur DM, Endress GA, Ebner R, Komatsoulis G;

XX Dian DR;

XX WPI: 2000-224656/19.

XX N-PDB; AAV26284.

XX Novel secreted proteins and corresponding DNA molecules that can be

XX used to prevent, treat and diagnose disease in humans, for example,

XX Alzheimer's, cancer, and immune disorders -

XX Claim 11: Page 357; 416pp; English.

XX The polynucleotide sequences given in AAV26281 to AAV26336 encode the

XX human secreted proteins given in AAV91346 to AAV91449. The human secreted

XX proteins can have activities based on the tissues and cells they are

XX expressed in. Examples of the activities are: neuroprotective; nootropic;

XX neuroleptic; anti-manic; cerebroprotective; immunomodulatory;

XX anti-microbial; cardiac; cytosolic; anti-inflammatory; haemostatic;

XX anticoagulant; and vasotropic. The polynucleotides and proteins may be

XX used to prevent, treat or ameliorate a medical condition, e.g. by protein

XX or gene therapy. Conditions treatable by the proteins of the invention

XX include neural, reproductive, or immune disorders, especially

XX immunodeficiency, infection, lymphomas, demyelinating diseases,

XX aneurysms and haemorrhages. Specific examples include: Alzheimer's

XX disease; Parkinson's; Huntington's; Tourette syndrome; multiple

XX sclerosis; meningitis; ischaemia; prostate cancer; mania; dementia;

XX obsessive compulsive disorder and viral prophylaxis. The polynucleotides

XX and proteins can also be used in the detection of disorders associated

CC with the function of the protein, for example, the detection of
 CC developmental disorders, sexually-linked disorders, or disorders of the
 CC cardiovascular system. They may also be used as food additives or
 CC preservatives. AAA26272 to AAA26280 and AAY91345 are sequences used in
 CC the exemplification of the present invention.

XX Sequence 189 AA:

Query Match 17.1%; Score 84; DB 21; Length 189;
 Best Local Similarity 100.0%; Pred. No. 11e-74;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRPAFLCLLMOALMPGCGGHEPTADRGCSAGCAGCSYLHATMKROAEACILRGCA 60

DB 1 mrpafalcllmoalmpgpggheptadrgcsagcagsylhahatmkrgaaeacilrgca 60

OY 61 LSTVAGAEIRAVLALLRAGPG 84

DB 61 lstrvagaeltavalllrpgpg 84

RESULT 12

AA91409

ID AAY91409 standard; Protein: 123 AA.

29-JUN-2000 (first entry)

Human secreted protein sequence encoded by gene 4 SEQ ID NO:130.

XX Human; secreted protein; diagnosis; neuroprotective; noctropic;
 KW neuroleptic; antimanic; cerebroprotective; immunomodulatory;
 KW anti-microbial; cardiant; cytostatic; antiinflammatory; haemostatic;
 KW anticonvulsant; vasotropic; vaccine; gene therapy; anti-sense therapy;
 KW neural; reproductive; immune disorder; immunodeficiency; infection;
 KW lymphoma; demyelinating disease; autoimmunity; cancer; inflammation;
 KW aneurysm; haemorrhage; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; Tourette syndrome; multiple sclerosis; meningitis;
 KW ischaemia; mania; dementia; obsessive compulsive disorder;
 KW viral prophylaxis; developmental disorder; sexually-linked disorder;
 KW cardiovascular disorder; food additive; preservative; chromosome 14.

XX Homo sapiens.

XX MO200011014-A1.

PD 02-MAR-2000.

XX 24-AUG-1999; 99WO-US19330.

XX 25-AUG-1998; 98US-0097917.

XX 31-AUG-1998; 98US-0098634.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Moore PA, Ruben SM, Olsen HS, Shi Y, Rosen CA, Florence KA;
 PI Soppet DR, Lafleur DW, Endress GA, Edner R, Komatsoulis G;
 PI Duan RD;

XX WPI: 2000-224656/19.

XX Novel secreted proteins and corresponding DNA molecules that can be
 PT used to prevent, treat and diagnose disease in humans, for example,
 PT Alzheimer's, cancer, and immune disorders -

XX Disclosure: Page 391; 416pp; English.

XX The polynucleotide sequences given in AAA26281 to AAA26336 encode the
 CC human secreted proteins given in AAY91346 to AAY91449. The human secreted
 CC proteins can have activities based on the tissues and cells they are
 CC expressed in. Examples of the activities are: neuroprotective; noctropic;

CC neuroleptic; antimanic; cerebroprotective; immunomodulatory;
 CC anti-microbial; cardiant; cytostatic; antiinflammatory; haemostatic;
 CC anticonvulsant; and vasotropic. The polynucleotides and proteins may be
 CC used to prevent, treat or ameliorate a medical condition, e.g. by protein
 CC or gene therapy. Conditions treatable by the proteins of the invention
 CC include neural, reproductive, or immune disorders, especially
 CC immunodeficiency, infection, lymphomas, demyelinating diseases,
 CC auto-immunities, cancer, general microbial infection, inflammation,
 CC aneurysms and haemorrhages. Specific examples include: Alzheimer's
 CC disease; Parkinson's; Huntington's; Tourette syndrome; multiple
 CC sclerosis; meningitis; ischaemia; prostate cancer; mania; dementia;
 CC obsessive compulsive disorder and viral prophylaxis. The polynucleotides
 CC and proteins can also be used in the detection of disorders associated
 CC with the function of the protein, for example, the detection of
 CC developmental disorders, sexually-linked disorders, or disorders of the
 CC cardiovascular system. They may also be used as food additives or
 CC preservatives. AAA26272 to AAA26280 and AAY91345 are sequences used in
 CC the exemplification of the present invention.

XX Sequence 123 AA:

Query Match 12.9%; Score 63; DB 21; Length 123;
 Best Local Similarity 100.0%; Pred. No. 4.7e-54;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 EHPTADRGCSAGCAGCSYLHATMKROAEACILRGALSTVAGAEIRAVLALLRAGP 81

DB 1 ehptadrgcsagcagsylhahatmkrgaaeacilrgalsstrvagaeltavalllrpg 60

OY 82 GPG 84

DB 61 gpg 63

RESULT 13

ABG08184

ID ABG08184 standard; Protein: 186 AA.

13-FEB-2002 (first entry)

Novel human diagnostic protein #8175.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HISE-) HYSEQ INC.

XX Dymnac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX N-PSDB: AAS72371.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 20; SEQ ID NO 38543; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 186 AA;
 Query Match
 Best Local Similarity 1.88; Score 9; DB 22; Length 186;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 RAGPQGGC 86;
 Db 139 ragpqp99g 147

RESULT 14

AAU54703 standard; Protein: 79 AA.

AC AAU54703;

XX 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #15599.

KW SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

PN W0200181581-A2.

XX 01-NOV-2001.

PF 20-APR-2001: 2001WO-US12865.

PR 21-APR-2000: 2000US-199047P.

PR 02-JUN-2000: 2000US-208841P.

PR 07-JUL-2000: 2000US-216747P.

XX (CORI-) CORIXA CORP.

PA Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A,
 PI L'Maisonneuve J, Zhang Y, Jen S, Carter D;

DR WPI: 2001-616774/71

DR N-PSDB: AAS5956.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris

PS Example 1; SEQ ID No 15898; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 79 AA;

Query Match
 Best Local Similarity 1.68; Score 8; DB 22; Length 79;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 ALERRRSH 102
 Db 20 alerrrrsh 27

RESULT 15

AAU43842 standard; Protein: 123 AA.

AC AAU43842;

XX 13-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #4738.

KW SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

PN W0200181581-A2.

XX 01-NOV-2001.

PF 20-APR-2001: 2001WO-US12865.

PR 21-APR-2000: 2000US-199047P.

PR 02-JUN-2000: 2000US-208841P.

PR 07-JUL-2000: 2000US-216747P.

XX (CORI-) CORIXA CORP.

PA Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A,
 PI L'Maisonneuve J, Zhang Y, Jen S, Carter D;

DR WPI: 2001-616774/71

DR N-PSDB: AAS59521.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2002, 09:37:56 ; Search time 30.68 Seconds
(without alignments)
2762.957 Million cell updates/sec

Title: US-09-902-713b-96

Perfect score: 490

Sequence: 1 MRPALCLLMQALMPGPG.....LDRAGCALAESPLGSSDA 490

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Wo size: 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database :

SPTREMBL.19:**
1: sp_archaea:**
2: sp_bacteria:**
3: sp_fungi:**
4: sp_human:**
5: sp_invertebrate:**
6: sp_mammal:**
7: sp_mhc:**
8: sp_organelle:**
9: sp_phage:**
10: sp_plant:**
11: sp_rodent:**
12: sp_virus:**
13: sp_vertebrate:**
14: sp_unclassified:**
15: sp_virus:**
16: sp_bacterioph:**
17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	158	32.2	212	4 Q9P096	Q9P096 homo sapien
2	24	4.9	459	11 Q9DC55	Q9DC55 mus musculu
3	24	4.9	459	11 Q9D624	Q9D624 mus musculu
4	24	4.9	459	11 Q9CXA8	Q9CXA8 mus musculu
5	8	1.6	187	2 Q9E0J8	Q9E0J8 salmonella
6	8	1.6	222	2 Q9ADC6	Q9ADC6 streptomyce
7	8	1.6	371	5 Q9VZS1	Q9VZS1 petromycon
8	8	1.6	438	13 Q9JLX3	Q9JLX3 dirosophila
9	8	1.6	464	11 Q9JLF3	Q9JLF3 petromycon
10	8	1.6	491	4 Q9NS54	Q9NS54 mus musculu
11	8	1.6	498	11 Q9JAS3	Q9JAS3 homo sapien
12	8	1.6	498	11 Q9JAS3	Q9JAS3 pseudomonas
13	8	1.6	730	12 Q9G634	Q9G634 mus musculu
14	8	1.6	1343	12 Q9G635	Q9G634 bovine herp
15	8	1.6	1816	16 Q9KBB4	Q9KBB4 bovine herp
16	8	1.6	1816	16 Q9KBB4	Q9KBB4 bacillus ha

17	7	1.4	72	12 Q69143	Q69143 human herpe
18	7	1.4	76	2 Q9AJX7	Q9AJX7 streptomyce
19	7	1.4	80	2 Q9EWN2	Q9EWN2 streptomyce
20	7	1.4	88	17 Q970G5	Q970G5 sulfolobus
21	7	1.4	92	2 Q9X7P3	Q9X7P3 streptomyce
22	7	1.4	97	10 Q49401	Q49401 arabidopsis
23	7	1.4	102	15 Q91931	Q91931 human immun
24	7	1.4	102	15 Q9YVG5	Q9YVG5 human immun
25	7	1.4	103	15 Q91930	Q91930 human immun
26	7	1.4	109	2 Q9ZNB8	Q9ZNB8 nitrosomona
27	7	1.4	115	6 Q9Z921	Q9Z921 sus scrofa
28	7	1.4	127	4 Q9B282	Q9B282 homo sapien
29	7	1.4	130	2 Q9ZB13	Q9ZB13 streptomyce
30	7	1.4	131	4 Q9H5Y0	Q9H5Y0 homo sapien
31	7	1.4	136	2 Q9X8S4	Q9X8S4 streptomyce
32	7	1.4	139	2 Q9XAP5	Q9XAP5 streptomyce
33	7	1.4	150	4 Q9S923	Q9S923 homo sapien
34	7	1.4	151	2 Q9K5J4	Q9K5J4 buchnera ap
35	7	1.4	151	2 Q9K5J3	Q9K5J3 buchnera ap
36	7	1.4	151	2 Q9K5J2	Q9K5J2 buchnera ap
37	7	1.4	151	2 Q9K5J1	Q9K5J1 buchnera ap
38	7	1.4	151	2 Q9K5J0	Q9K5J0 buchnera ap
39	7	1.4	151	2 Q9K5I9	Q9K5I9 buchnera ap
40	7	1.4	151	2 Q9K5I8	Q9K5I8 buchnera ap
41	7	1.4	151	2 Q9K5I7	Q9K5I7 buchnera ap
42	7	1.4	151	2 Q9K5I6	Q9K5I6 buchnera ap
43	7	1.4	151	2 Q9K5I5	Q9K5I5 buchnera ap
44	7	1.4	151	2 Q9K5I4	Q9K5I4 buchnera ap
45	7	1.4	151	2 Q9K5I3	Q9K5I3 buchnera ap
46	7	1.4	151	2 Q9K5I2	Q9K5I2 buchnera ap
47	7	1.4	151	2 Q9K5I1	Q9K5I1 buchnera ap
48	7	1.4	151	2 Q9K5C8	Q9K5C8 secondary e
49	7	1.4	151	2 Q9K5C6	Q9K5C6 secondary e
50	7	1.4	151	2 Q9K5C5	Q9K5C5 secondary e
51	7	1.4	151	2 Q9K5C4	Q9K5C4 secondary e
52	7	1.4	151	11 Q91VW0	Q91VW0 mus musculu
53	7	1.4	152	12 Q9DUD0	Q9DUD0 tt virus
54	7	1.4	155	4 Q96G14	Q96G14 homo sapien
55	7	1.4	155	16 Q920X5	Q920X5 rhizobium m
56	7	1.4	161	5 Q9GPG6	Q9GPG6 trypanosoma
57	7	1.4	161	5 Q9DUD0	Q9DUD0 leishmania
58	7	1.4	166	2 Q87504	Q87504 escherichia
59	7	1.4	172	14 Q991W0	Q991W0 uncultured
60	7	1.4	173	2 P72384	P72384 streptomyce
61	7	1.4	180	2 Q9R1T9	Q9R1T9 streptomyce
62	7	1.4	180	15 Q91872	Q91872 human immun
63	7	1.4	190	16 Q9RMB3	Q9RMB3 deinoococcus
64	7	1.4	191	16 Q9A6B2	Q9A6B2 caulobacter
65	7	1.4	191	17 Q9YF50	Q9YF50 aeropyrum p
66	7	1.4	193	4 Q92605	Q92605 homo sapien
67	7	1.4	195	11 Q60539	Q60539 mesocricetu
68	7	1.4	198	4 Q12870	Q12870 homo sapien
69	7	1.4	199	4 Q9N001	Q9N001 homo sapien
70	7	1.4	203	4 Q13222	Q13222 homo sapien
71	7	1.4	207	10 Q9S903	Q9S903 arabidopsis
72	7	1.4	212	17 Q9Y9C9	Q9Y9C9 aeropyrum p
73	7	1.4	213	16 Q9RYD3	Q9RYD3 mus musculu
74	7	1.4	214	11 Q9D0P3	Q9D0P3 mus musculu
75	7	1.4	216	5 P90877	P90877 caenorhabdi
76	7	1.4	217	11 Q9C8S4	Q9C8S4 mus musculu
77	7	1.4	218	16 Q985B5	Q985B5 rhizobium l
78	7	1.4	223	16 Q9RUD8	Q9RUD8 deinoococcus
79	7	1.4	228	11 Q70473	Q70473 cricetus
80	7	1.4	230	10 Q94J39	Q94J39 oryza sativ
81	7	1.4	240	2 Q9RGE7	Q9RGE7 clostridium
82	7	1.4	242	2 Q938N5	Q938N5 streptococc
83	7	1.4	243	16 Q9RX66	Q9RX66 deinoococcus
84	7	1.4	246	2 Q9K431	Q9K431 streptomyce
85	7	1.4	249	16 Q9AAW0	Q9AAW0 caulobacter
86	7	1.4	252	11 Q9CT53	Q9CT53 mus musculu
87	7	1.4	252	11 Q9C0I5	Q9C0I5 mus musculu
88	7	1.4	253	16 Q9RYD6	Q9RYD6 deinoococcus
89	7	1.4	254	5 Q27230	Q27230 taenia ovis

DR MGD:1914114; 1200003C23R1K.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001304; lectin_c.
 DR SMART: SM00034; CLECT. 1.
 DR SMART: SM00181; EGF. 1.
 DR SMART: SM00001; EGF-like. 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN.1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 SO SEQUENCE 459 AA; 49053 MW; 6CB25D048A456A7B CRC64;

Query Match 4.9%; Score 24; DB 11; Length 459;
 Best Local Similarity 100.0%; Pred. No. 3.4e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 GYLCKYQFVLCPPAPRGASNS 191
 DB 168 GYLCKYQFVLCPPAPRGASNS 191

AC 09D624 PRELIMINARY; PRT; 459 AA.
 AC 09D624;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE 1200003C23R1K PROTEIN.
 GN 1200003C23R1K
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=HEAD;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyszynski-Bolis A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK014681; BAB29502.1; -
 DR HSSP: P00743; 1CCF.
 DR MGD: MGI:1914114; 1200003C23R1K.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001304; lectin_c.
 DR SMART: SM00034; CLECT. 1.
 DR SMART: SM00181; EGF. 1.
 DR SMART: SM00001; EGF-like. 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN.1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 SO SEQUENCE 459 AA; 49065 MW; A257B38DA598EC8A CRC64;

Query Match 4.9%; Score 24; DB 11; Length 459;

Best Local Similarity 100.0%; Pred. No. 3.4e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 GYLCKYQFVLCPPAPRGASNS 191
 DB 168 GYLCKYQFVLCPPAPRGASNS 191

AC 09CXAB PRELIMINARY; PRT; 459 AA.
 AC 09CXAB;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE 1200003C23R1K PROTEIN.
 GN 1200003C23R1K
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRIONIC LUNG;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyszynski-Bolis A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK014632; BAB31209.1; -
 DR HSSP: P00743; 1CCF.
 DR MGD: MGI:1914114; 1200003C23R1K.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001304; lectin_c.
 DR SMART: SM00034; CLECT. 1.
 DR SMART: SM00181; EGF. 1.
 DR SMART: SM00001; EGF-like. 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN.1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 SO SEQUENCE 459 AA; 49150 MW; A649730F15132DCD CRC64;

Query Match 4.9%; Score 24; DB 11; Length 459;
 Best Local Similarity 100.0%; Pred. No. 3.4e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 GYLCKYQFVLCPPAPRGASNS 191
 DB 168 GYLCKYQFVLCPPAPRGASNS 191

AC 09EUJ8 PRELIMINARY; PRT; 187 AA.
 AC 09EUJ8;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)

01-MAR-2001 (TREMblrel. 16, Last sequence update)
 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 ORF27 (CONJUGATIVE TRANSFER: REGULATION)
 FINO.
 Salmomella enterica subsp. enterica serovar Choleraesuis, and
 Salmomella typhimurium LT2.
 Plasmid 50k virulence plasmid, and plasmid pSLT.
 Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Salmomella.
 NCBI_TaxID=119912, 99287;
 [1]
 SEQUENCE FROM N.A.
 SPECIES=S. typhimurium LT2; STRAIN=SGSC1412; PLASMID=PSLT;
 PLASMID=50k VIRULENCE PLASMID;
 MEDLINE=21153631; PubMed=11254626;
 Handed T., Okada N., Nakazawa N., Kawakami T., Danbara H.,
 RT Complete DNA Sequence and Comparative Analysis of the 50-kilobase
 virulence plasmid of Salmomella enterica serovar Choleraesuis.";
 Infect. Immun. 69:2612-2620(2001).
 [2]
 SEQUENCE FROM N.A.
 SPECIES=S. typhimurium LT2; STRAIN=SGSC1412; PLASMID=PSLT;
 WASHU:
 "The Salmomella typhimurium Genome Sequencing Project."
 Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 [3]
 SEQUENCE FROM N.A.
 SPECIES=S. typhimurium LT2; STRAIN=SGSC1412; PLASMID=PSLT;
 McClelland M., Sanderson K., Spieth J., Clifton S., Latreille P.,
 RA Courtney L., All J., Dane M., Du F., Hou S., Layman D., Leonard S.,
 RA Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E.,
 RA Sun H., Florea L., Miller W., Porwollik S., Stoneking T., Nhan M.,
 RL Waterston R., Wilson R.,
 DR Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB040415; BAB20534.1;
 DR EMBL: AC006471; AAL23511.1;
 DR HSP: P29367; IDVO.
 KW Plasmid.
 SQ SEQUENCE 187 AA; 21133 MW; D6E2D389CAEE9EB8 CRC64;

Query Match
 Best Local Similarity 1.6%; Score 8; DB 2; Length 187;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 66 AELRAVLA 75
 11111111
 177 AELRAVLA 184

RESULT 6
 ID 09ADC6 PRELIMINARY; PRT; 222 AA.
 AC 09ADC6;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 GN SP2A2 PROTEIN
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
 NCBI_TaxID=11902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Saunders D.C., Harris D.,
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RN Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

09VZS1
 ID 09VZS1 PRELIMINARY; PRT; 371 AA.
 AC 09VZS1;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-OCT-2001 (TREMblrel. 18, Last annotation update)
 GN CG17746
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 SQ SEQUENCE 222 AA; 23251 MW; B74F3719B4BF310A CRC64;

Query Match
 Best Local Similarity 1.6%; Score 8; DB 2; Length 222;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 444 ESDEPAA 451
 11111111
 Db 141 ESDEPAA 148

RESULT 7
 ID 090Y00 PRELIMINARY; PRT; 284 AA.
 AC 090Y00;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 GN STERIOD RECEPTOR (FRAGMENT)
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 NCBI_TaxID=7757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Escriva H., Manzoni L., Youson J., Laudet V.;
 RT "Analysis of cyclostone genes reveals waves of gene duplication during
 early vertebrate evolution."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF16879; AAL26247.1;
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 284 284
 SQ SEQUENCE 284 AA; 32284 MW; 6E6DC2PC07F27C27 CRC64;

Query Match
 Best Local Similarity 1.6%; Score 8; DB 13; Length 284;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 383 TTSSATPQ 390
 11111111
 Db 63 TTSSATPQ 70

RESULT 8
 ID 09VZS1 PRELIMINARY; PRT; 371 AA.
 AC 09VZS1;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-OCT-2001 (TREMblrel. 18, Last annotation update)
 GN CG17746
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 SQ SEQUENCE 222 AA; 23251 MW; B74F3719B4BF310A CRC64;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2002, 09:37:01 ; Search time 16.1 Seconds

(without alignments)
743.388 Million cell updates/sec

Title: US-09-902-713B-96

Perfect score: 490

Sequence: 1 MRPAFALCLIMQALWPGGG.....LRDRAGALLAESPLGSSDA 490

Scoring table:

OLIGO
Gapop 60.0, Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Wc size: 0

TC: number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 150 summaries

Database:

1: /cgn2.6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2.6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2.6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2.6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2.6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2.6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.6	234	1	US-08-299-567-5
2	8	1.6	238	1	US-08-240-124-2
3	8	1.6	238	1	US-08-453-943-2
4	8	1.6	238	2	US-09-057-121-2
5	8	1.6	238	4	US-09-358-734-2
6	7	1.4	330	2	US-08-712-948-2
7	7	1.4	333	2	US-08-712-948-1
8	7	1.4	834	4	US-09-143-571-29
9	7	1.4	1239	4	US-08-937-931-2
10	7	1.4	1239	4	US-09-285-502-2
11	7	1.4	1239	4	US-09-709-126-2
12	7	1.4	2089	4	US-08-418-893D-23
13	7	1.4	2089	1	US-08-418-893D-20
14	6	1.2	14	1	US-08-445-745-120
15	6	1.2	15	1	US-08-447-010-21
16	6	1.2	15	1	US-07-859-291C-37
17	6	1.2	18	2	US-08-124-981A-30
18	6	1.2	18	3	US-09-037-190-26
19	6	1.2	18	3	US-09-037-192-26
20	6	1.2	18	4	US-09-037-143-26
21	6	1.2	18	4	US-09-049-691-26
22	6	1.2	18	4	US-08-260-174-26
23	6	1.2	18	4	US-09-338-128A-26
24	6	1.2	18	4	US-09-232-346-26
25	6	1.2	20	2	US-08-124-981A-26
26	6	1.2	20	2	US-09-010-928B-7
27	6	1.2	23	3	US-08-855-531D-38

28	6	1.2	23	4	US-08-855-526B-38	Sequence 38, Appl
29	6	1.2	24	4	US-09-439-897-62	Sequence 62, Appl
30	6	1.2	25	2	US-08-902-516-4	Sequence 4, Appl
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35	6	1.2	36	1	US-08-428-248-4	Sequence 4, Appl
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125	6	1.2	240	3	US-08-077-253-4	Sequence 4, Appl
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136	6	1.2	272	4	US-09-151-083-26	Sequence 2, Appl
137	6	1.2	273	4	US-09-085-104-1	Sequence 26, Appl
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139	6	1.2	288	2	US-08-737-825-8	Sequence 16, Appl
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141	6	1.2	293	3	US-09-037-190-51	Sequence 62, Appl
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143	6	1.2	293	4	US-09-037-143-51	Sequence 51, Appl
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145	6	1.2	293	4	US-08-260-174-51	Sequence 51, Appl
146	6	1.2	293	4	US-09-338-128A-51	Sequence 51, Appl
147	6	1.2	293	4	US-09-332-346-51	Sequence 51, Appl
148	6	1.2	297	1	US-08-534-910B-6	Sequence 6, Appl
149	6	1.2	297	1	US-08-534-910B-8	Sequence 8, Appl
150	6	1.2	297	1	US-08-534-910B-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-299-567-5
Sequence 5, Application US/08299567
Patent No. 5747033

GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
NUMBER OF SEQUENCES: 8
ACTIVITY OF EPH FAMILY LIGANDS
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,567
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kempier, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 290
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-299-567-5

Query Match 1.6% Score 8; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 79 AGGPGGG 86
Db 71 AGGPGGG 78

RESULT 2
US-08-240-124-2
Sequence 2, Application US/08240124
Patent No. 5516658
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:

GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2002, 09:36:21 ; Search time 20.98 Seconds
(without alignments)
2244.222 Million cell updates/sec

Title: US-09-902-713b-96

Perfect score: 490
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size: 0

Number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database: PIR71:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	8	1.6	1041	2 S55862	probable membrane
5	8	1.6	1816	2 F83901	hypothetical prote
6	8	1.4	55	2 AH2074	hypothetical prote
7	7	1.4	76	2 AG3389	hypothetical prote
8	7	1.4	92	2 T35262	hypothetical prote
9	7	1.4	97	2 G85212	hypothetical prote
10	7	1.4	113	2 T05023	hypothetical prote
11	7	1.4	130	2 T35978	hypothetical prote
12	7	1.4	133	2 S58123	thiorodoxin (clone
13	7	1.4	134	2 147010	gasftrin-releasing
14	7	1.4	136	2 T36547	hypothetical prote
15	7	1.4	139	2 T34633	hypothetical prote
16	7	1.4	151	2 S37647	H+-transporting AT
17	7	1.4	190	2 H75478	conserved hypothet
18	7	1.4	191	2 F72731	hypothetical prote
19	7	1.4	191	2 E87519	Thyl/PlpI family P
20	7	1.4	198	2 A57717	transcription fact
21	7	1.4	207	2 E86429	hypothetical prote
22	7	1.4	212	2 C72464	hypothetical prote
23	7	1.4	213	2 F75585	urease accessory p
24	7	1.4	213	2 B84333	isopenicillin pyrph
25	7	1.4	216	2 T22314	hypothetical prote
26	7	1.4	223	2 G75394	conserved hypothet
27	7	1.4	238	2 S03906	45k antigen - shee
28	7	1.4	243	2 E75517	hypothetical prote
29	7	1.4	249	2 B87309	hypothetical prote

30	7	1.4	253	2 E75570	gldb protein - Del
31	7	1.4	259	2 T49596	related to H+-tran
32	7	1.4	264	2 E83284	probable enoyl-CoA
33	7	1.4	268	2 A72552	hypothetical prote
34	7	1.4	268	2 A12212	hypothetical prote
35	7	1.4	269	2 T36001	probable integral
36	7	1.4	270	2 S65739	basigin precursor
37	7	1.4	278	2 C86421	FIN18.17 protein -
38	7	1.4	290	2 G71304	probable translati
39	7	1.4	290	2 A69779	conserved hypothet
40	7	1.4	293	2 T09758	myb-related protei
41	7	1.4	302	2 H82638	hypothetical prote
42	7	1.4	309	2 E64224	yabc protein homol
43	7	1.4	312	2 T43853	conserved hypothet
44	7	1.4	312	2 AH2389	hypothetical prote
45	7	1.4	313	2 D86829	ribose ABC transpo
46	7	1.4	313	2 C69321	conserved hypothet
47	7	1.4	318	1 S30914	2-desacetyl-2-hydr
48	7	1.4	318	1 T50752	2-desacetyl-2-hydr
49	7	1.4	325	1 A33851	alcohol dehydrogen
50	7	1.4	328	2 S35336	transcription fact
51	7	1.4	330	2 A40855	homeotic protein H
52	7	1.4	339	2 F83026	conserved hypothet
53	7	1.4	344	2 G71858	udp-glucose 4-epim
54	7	1.4	345	2 D91201	type III secretion
55	7	1.4	345	2 H86047	glutamate decarbox
56	7	1.4	352	2 D84192	hypothetical prote
57	7	1.4	360	2 D65045	hypothetical prote
58	7	1.4	360	2 H91068	hypothetical prote
59	7	1.4	360	2 B85813	hypothetical prote
60	7	1.4	376	2 S69529	thiamin biosynthes
61	7	1.4	377	2 AC0933	hypothetical prote
62	7	1.4	383	2 AD0504	hypothetical prote
63	7	1.4	401	2 G83197	probable acyl-CoA
64	7	1.4	411	2 B97309	probable Mn transp
65	7	1.4	412	2 AB2471	hypothetical prote
66	7	1.4	418	2 H81383	glycine hydroxymet
67	7	1.4	418	2 T29470	hypothetical prote
68	7	1.4	423	2 H83603	hypothetical prote
69	7	1.4	433	2 C88594	protein Y48A6B.10
70	7	1.4	439	2 I57561	transcription fact
71	7	1.4	446	2 T26988	hypothetical prote
72	7	1.4	449	2 G95004	competence factor
73	7	1.4	451	2 D69356	serine hydroxymet
74	7	1.4	451	1 XUBHFG	flavonol 3-O-gluc
75	7	1.4	458	2 C82952	ATP synthase beta
76	7	1.4	460	1 PMECB	H+-transporting tw
77	7	1.4	460	2 B91213	H+-transporting AT
78	7	1.4	460	2 C86059	ATP synthase beta
79	7	1.4	460	2 AF0954	H+-transporting AT
80	7	1.4	460	2 AE0500	ATP synthase beta
81	7	1.4	461	2 G86594	lipamide dehydrog
82	7	1.4	461	2 C72031	2-oxo acid dehydro
83	7	1.4	461	2 C64796	dec. protein
84	7	1.4	461	2 D90711	c4-dicarboxylate a
85	7	1.4	461	2 H85561	transport of dicar
86	7	1.4	461	2 AF0579	H+-transporting AT
87	7	1.4	462	2 S06082	ATP synthase, beta
88	7	1.4	467	2 F82036	ATP synthase FI, b
89	7	1.4	467	2 T34874	hypothetical prote
90	7	1.4	468	2 D64071	H+-transporting AT
91	7	1.4	465	2 G81024	ATP synthase FI, b
92	7	1.4	466	2 G82715	ATP synthase, beta
93	7	1.4	467	2 S06082	H+-transporting AT
94	7	1.4	467	2 F82036	ATP synthase FI, b
95	7	1.4	468	2 T34874	hypothetical prote
96	7	1.4	468	2 D64071	H+-transporting AT
97	7	1.4	477	2 T23598	hypothetical prote
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102	7	1.4	506	2 S36494	E2 protein - human
				2 F83547	sodium/proline sym

103	7	1.4	507	2	G01614	zinc finger protei
104	7	1.4	509	2	S76731	hypothetical prote
105	7	1.4	510	1	W3BE47	protein-serine/thr
106	7	1.4	540	2	G50068	choline transpor
107	7	1.4	549	2	T23526	hypothetical prote
108	7	1.4	561	2	G68837	nodulin-like prote
109	7	1.4	563	2	T36704	probable dehydrog
110	7	1.4	567	2	A86262	hypothetical prote
111	7	1.4	579	2	T24880	hypothetical prote
112	7	1.4	584	2	T29469	hypothetical prote
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114	7	1.4	605	2	AH1150	ABC transporter, A
115	7	1.4	605	2	A11509	probable branched
116	7	1.4	608	2	T35755	threonyl-tRNA synt
117	7	1.4	611	2	D70928	hypothetical prote
118	7	1.4	640	2	F83303	hypothetical prote
119	7	1.4	647	2	S67651	MPS1 protein - mou
120	7	1.4	661	2	I52603	hypothetical prote
121	7	1.4	674	2	D72329	probable penicilli
122	7	1.4	678	2	B70913	potassium transpor
123	7	1.4	690	2	A83441	tryptophan synthas
124	7	1.4	702	1	JU0401	ATP-dependent tran
125	7	1.4	724	2	D48941	hypothetical prote
126	7	1.4	738	2	D70680	epithelial microtu
127	7	1.4	749	2	I37356	probable two-compo
128	7	1.4	797	2	G83570	monocyte surface a
129	7	1.4	826	2	A60385	RED1 protein - yea
130	7	1.4	827	1	COBYD1	trac protein homol
131	7	1.4	856	2	T31234	collagen alpha 2 c
132	7	1.4	991	2	T01372	hypothetical prote
133	7	1.4	1051	2	A35763	probable disintegr
134	7	1.4	1076	2	F96831	hypothetical prote
135	7	1.4	1239	2	T13809	hypothetical prote
136	7	1.4	1312	2	T22738	DNA-directed RNA p
137	7	1.4	1487	2	T02850	hypothetical prote
138	7	1.4	1530	1	S01393	hypothetical prote
139	7	1.4	1642	2	T19130	hypothetical prote
140	7	1.4	1744	2	F61611	hypothetical prote
141	7	1.4	2089	1	A48757	acetyl-CoA carboxy
142	7	1.4	2475	2	T00047	gellan lyase (EC 4
143	7	1.4	3421	1	W2BE6	367k lequment prot
144	7	1.4	4151	2	T13734	LDL-receptor-relat
145	7	1.4	4753	2	T14593	springomyelin synth
146	7	1.4	9376	2	T14593	T-cell receptor J-
147	7	1.4	24	2	S40371	thymactin-like pro
148	6	1.2	26	2	T04371	hypothetical prote
149	6	1.2	45	2	T35208	
150	6	1.2				

ALIGNMENTS

RESULT 1

I38849

LEKR-3 - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999

C:Accession: I38849

R:Kozlovsky, C.J.; Marraskovsky, E.; McGrew, J.T.; Vandenbos, T.; Teepe, M.; Lyman, S.D.;

Oncogene 10, 299-306, 1995

A:Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encod

A:Reference number: I38849; MUID:95140419

A:Accession: I38849

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-238 <RES>

A:Cross-references: EMBL:U14187, NID:9642832; PIDN:AA050078.1; PTD:9642833

C:Genetics:

A:Gene: GDB:EP1G3

A:Cross-references: GDB:438336; OMIM:601381

A:Map position: 1q21-1q22

A:Family: axon guidance signal protein

Query Match

Best Local Similarity 1.6%; Score 8; DB 2; Length 238;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AGPGGGG 86

DB 75 AGPGGGG 82

RESULT 2

JC4374

sterol uptake protein 1 - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein G1828; protein YGL162w; SUT1 protein

C:Species: Saccharomyces cerevisiae

C>Date: 10-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 15-Sep-2000

C:Accession: JC4374; S60424; S64178

R:Bourol, S.; Karst, F.

Gene 165, 97-102, 1995

A:Title: Isolation and characterization of the Saccharomyces cerevisiae SUT1 gene inv

A:Reference number: JC4374; MUID:96084960

A:Accession: JC4374

A:Molecule type: DNA

A:Residues: 1-299 <BOU>

A:Cross-references: EMBL:X77766; NID:91183994; PIDN:CAAS4806.1; PID:91183995

R:James, C.M.; Indge, K.J.; Oliver, S.G.

Yeast 11, 1413-1419, 1995

A:Title: DNA sequence analysis of a 35 kb segment from Saccharomyces cerevisiae chrom

A:Reference number: S60417; MUID:96158061

A:Accession: S60424

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-299 <JAM>

A:Cross-references: EMBL:Z48618

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995

R:James, C.M.; Indge, K.J.; Oliver, S.G.

Submitted to the Protein Sequence Database, May 1996

A:Reference number: S64165

A:Accession: S64178

A:Molecule type: DNA

A:Residues: 1-299 <JAM>

A:Cross-references: EMBL:Z72684; NID:91322757; PID:e243599; PID:91322758; MIPS:YGL162

A:Experimental source: strain S288C

C:Comment: This protein is a member of the hypoxic gene family, and is rich in serine

C:Genetics:

A:Gene: SGP:SUT1

A:Cross-references: SGP:S0003130; MIPS:YGL162w

A:Map position: 7L

C:Superfamily: Saccharomyces cerevisiae hypothetical protein YPR009w

F:133-151/Region: serine/threonine-rich

Query Match

Best Local Similarity 1.6%; Score 8; DB 2; Length 299;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 NSTSSAT 388

DB 138 NSTSSAT 145

RESULT 3

T46915

hypothetical protein DKFZP762A227.1 - human

C:Species: Homo sapiens (man)

C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: T46915

R:Ottewill, B.; Obermaier, B.; Mewes, H.W.; Weil, B.; Wiemann, S.

Submitted to the Protein Sequence Database, February 2000

A:Reference number: Z24136

A:Accession: T46915

GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2002, 09:39:11 ; Search time 13.5 Seconds
(without alignments)
1405.376 Million cell updates/sec

US-09-902-713b-96

Title: Perfect score: 490

Sequence: 1 MKPAPALCLIMQALMPGPGG.....LRDRAEGALLAESPLGSSDA 490

Scoring table: OLIGO
Gapop 60.0 ; Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size: 0

Number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database: SwissProt_40:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.6	238	1	ERN3_HUMAN
2	8	1.6	299	1	SOT1_YEAST
3	8	1.6	1041	1	EGT2_YEAST
4	7	1.4	133	1	THH2_ARATH
5	7	1.4	134	1	GRE_SHEEP
6	7	1.4	155	1	MOAE_RHIME
7	7	1.4	192	1	YAGC_RHISN
8	7	1.4	213	1	ID1_HALNI
9	7	1.4	240	1	45KD_TAEVY
10	7	1.4	270	1	BASI_RABIT
11	7	1.4	290	1	EFPS_TREPA
12	7	1.4	309	1	Y222_MYCGE
13	7	1.4	318	1	BCHC_RHOSH
14	7	1.4	324	1	ALDX_HUMAN
15	7	1.4	324	1	ALDX_PIG
16	7	1.4	324	1	ALDX_RAT
17	7	1.4	325	1	YGAT_ECOLI
18	7	1.4	328	1	CEBB_CHICK
19	7	1.4	330	1	HX11_HUMAN
20	7	1.4	376	1	THH1_SALTY
21	7	1.4	376	1	Y023_BHPI
22	7	1.4	414	1	GLYA_CAME
23	7	1.4	416	1	PROA_LEPIN
24	7	1.4	431	1	SMA6_CHICK
25	7	1.4	449	1	COMB_STRPN
26	7	1.4	451	1	GLYA_ARCPN
27	7	1.4	455	1	UFGC_HORVU
28	7	1.4	457	1	ATPB_HAEIN
29	7	1.4	457	1	ATPB_PASWU
30	7	1.4	459	1	ATPB_ECOLI
31	7	1.4	461	1	DCUC_ECOLI
32	7	1.4	461	1	DLDH_CHLPPN
33	7	1.4	463	1	ATPB_BURCE

34	7	1.4	465	1	ATPB_BUCAL
35	7	1.4	466	1	ATPB_BUCAP
36	7	1.4	466	1	ATPB_VIBAL
37	7	1.4	466	1	ATPB_VIBCH
38	7	1.4	468	1	ATPB_THREE
39	7	1.4	482	1	RI67_YEAST
40	7	1.4	502	1	VE2_HPV25
41	7	1.4	507	1	MKR3_HUMAN
42	7	1.4	510	1	KR2_VZVD
43	7	1.4	510	1	INW2_DAUCA
44	7	1.4	592	1	Y713_MYCTU
45	7	1.4	611	1	DUS8_HUMAN
46	7	1.4	625	1	AMT_ALTRA
47	7	1.4	669	1	NAD6_MYCTU
48	7	1.4	679	1	FZD8_MOUSE
49	7	1.4	685	1	ATRB_PSEAE
50	7	1.4	690	1	TRP_COPCI
51	7	1.4	702	1	TRP_COPCI
52	7	1.4	724	1	PEPD_PEDOC
53	7	1.4	826	1	ADOB_MOUSE
54	7	1.4	827	1	CADG_HUMAN
55	7	1.4	829	1	MSH5_HUMAN
56	7	1.4	834	1	Y419_HUMAN
57	7	1.4	991	1	TLR9_HUMAN
58	7	1.4	1032	1	TLR9_MOUSE
59	7	1.4	1032	1	T2D3_HUMAN
60	7	1.4	1083	1	TP3A_DROME
61	7	1.4	1250	1	PUR4_HUMAN
62	7	1.4	1338	1	RPC1_TRYBB
63	7	1.4	1530	1	Y419_HUMAN
64	7	1.4	1544	1	TUSP_HUMAN
65	7	1.4	1547	1	TUSP_MOUSE
66	7	1.4	1547	1	TREG_HSVB
67	7	1.4	3421	1	LRP_CABEL
68	7	1.4	4753	1	TAT_HV128
69	7	1.2	14	1	TAT_HV123
70	7	1.2	47	1	LHA2_ECTHA
71	7	1.2	49	1	PSBU_SYNGU
72	7	1.2	50	1	KO2_CAEEL
73	7	1.2	55	1	SECE_THEMA
74	7	1.2	65	1	HPIS_PARSP
75	7	1.2	71	1	BB13_SCHCO
76	7	1.2	73	1	Y4HR_RHISN
77	7	1.2	74	1	NEUG_BOVIN
78	7	1.2	76	1	NEUG_CAPHI
79	7	1.2	78	1	NEUG_HUMAN
80	7	1.2	78	1	NEUG_RAT
81	7	1.2	83	1	RL27_THDMA
82	7	1.2	86	1	ISK4_MOUSE
83	7	1.2	86	1	TAT_HV126
84	7	1.2	91	1	Y97_ADE07
85	7	1.2	92	1	Y36_ARCFU
86	7	1.2	98	1	SRG1_MOUSE
87	7	1.2	98	1	SRG1_RAT
88	7	1.2	99	1	TAT_HV126
89	7	1.2	101	1	TAT_HV126
90	7	1.2	103	1	EMF1_CHICK
91	7	1.2	103	1	Y688_HAEIN
92	7	1.2	104	1	BCHA_HERYP
93	7	1.2	107	1	SSIS_STRFR
94	7	1.2	107	1	VLI_FVYL
95	7	1.2	110	1	YH07_YEAST
96	7	1.2	111	1	DAD1_DROME
97	7	1.2	112	1	FRT2_HUMAN
98	7	1.2	113	1	GUAN_HUMAN
99	7	1.2	115	1	HY44_MOUSE
100	7	1.2	115	1	NU3M_ONCGO
101	7	1.2	116	1	NU3M_ONCKE
102	7	1.2	116	1	NU3M_ONCKI
103	7	1.2	116	1	NU3M_ONCMA
104	7	1.2	116	1	NU3M_ONCMY
105	7	1.2	116	1	NU3M_ONCNE
106	7	1.2	116	1	NU3M_ONCTS

P57124	buchnera ap
Q07232	buchnera ap
P12986	vibrio algi
Q9knh5	vibrio chol
P41168	thiobacilli
P39743	saccharomyc
P36787	human papil
Q13064	homo sapien
P09286	varicella-z
Q39692	daucus caro
Q10830	mycobacteri
Q13202	homo sapien
P29957	alteromonas
P71911	mycobacteri
Q61091	mus musculu
P57658	pseudomonas
P16578	coprinus cl
P36497	pediococcus
Q05910	mus musculu
P14291	saccharomyc
Q75309	homo sapien
Q43196	homo sapien
Q43303	homo sapien
Q9nr36	homo sapien
Q9eqn3	mus musculu
Q00268	homo sapien
Q9ng98	drosophila
O15067	homo sapien
P08968	trypanosoma
Q9nr14	homo sapien
Q9nj15	mus musculu
P28955	equine herp
Q04833	caenorhabdi
P12511	human immun
P12510	human immun
P80101	ecoli
P34297	caenorhabdi
P56152	synechococc
P35874	thermotoga
P00264	paracoccus
P37444	schizophyll
P55482	rhizobium s
P35722	bos taurus
P54877	capra hircu
Q92686	homo sapien
Q04940	rattus norv
Q9x197	thermotoga
Q35679	mus musculu
P12506	human immun
P04509	human immun
P05668	human adeno
Q28637	archaeoglob
Q88745	mus musculu
Q92865	rattus norv
P04611	human immun
P19552	human immun
P08317	gallus gall
P44037	haemophilus
P26277	erythrobact
Q91643	streptomyces
P06456	avian papil
P38804	saccharomyc
Q9vln5	drosophila
Q75441	homo sapien
Q02747	homo sapien
P01820	mus musculu
P20666	oncorhynch
Q35262	oncorhynch
P20667	oncorhynch
Q37168	oncorhynch
P11629	oncorhynch
P20668	oncorhynch
P25707	oncorhynch

107	6	1.2	116	1	NU3M_SALSA	035929	salmo salar
108	6	1.2	116	1	NU3M_SALTR	003852	salmo trutt
109	6	1.2	118	1	YRP4_IRPV6	P18808	chilo lride
110	6	1.2	118	1	B2MG_HUMAN	P01884	homo sapien
111	6	1.2	119	1	B2MG_PONPY	P16213	pongo pygma
112	6	1.2	120	1	YPH5_CHRVI	P45374	chromotium
113	6	1.2	122	1	RL7_HALEU	P07472	halophilic
114	6	1.2	122	1	YG27_YEAST	P53340	saccharomyc
115	6	1.2	123	1	EP4_RABIT	Q28631	oryctolagus
116	6	1.2	123	1	MIR1_HUMAN	O99616	homo sapien
117	6	1.2	123	1	RR12_SPIKX	P42344	spirogyra m
118	6	1.2	125	1	GAMD_DROME	O99812	drosophila
119	6	1.2	125	1	YCD6_HUMAN	O99347	homo sapien
120	6	1.2	126	1	YMO6_SULSO	O97u19	sulfolobus
121	6	1.2	129	1	CCDP_MAIZE	O01595	zea mays (m
122	6	1.2	130	1	OREX_MOUSE	O05241	mus musculu
123	6	1.2	130	1	OREX_MOUSE	O05232	rattus norv
124	6	1.2	133	1	R35A_AERPE	O99944	aeropyrum p
125	6	1.2	133	1	FLGC_SALTY	P16438	salmonella
126	6	1.2	134	1	Y6C6_ECOLI	O47719	escherichia
127	6	1.2	137	1	YL99_MYCTU	O10406	mycobacteri
128	6	1.2	139	1	HBA_BRARE	O90487	brachydario
129	6	1.2	142	1	HBA_CARAU	P02018	carassius a
130	6	1.2	142	1	HBA_CARAU	P02017	catostomus
131	6	1.2	143	1	ATXA_STRCL	P01551	streptomyce
132	6	1.2	143	1	CGGA_STRCL	O06110	streptomyce
133	6	1.2	143	1	GSFG_XANCP	P31734	xanthomonas
134	6	1.2	144	1	HV43_MOUSE	P01819	mus musculu
135	6	1.2	146	1	SLYA_ECOLI	P55740	escherichia
136	6	1.2	147	1	SLYA_SALTY	P02676	salmonella
137	6	1.2	147	1	HBB_CARAU	P02417	bacillus st
138	6	1.2	149	1	RL9_BACSF	O35142	rhodobacter
139	6	1.2	153	1	C554_RHOSH	O957n7	arabidopsis
140	6	1.2	160	1	PSAG_ARATH	O06118	streptomyce
141	6	1.2	165	1	PPI_STRCH	O95818	hordeum vul
142	6	1.2	168	1	TCTP_HORVU	O26917	methanobact
143	6	1.2	170	1	BM4E_ECOLI	O92K14	helicobacte
144	6	1.2	171	1	LE23_METTH	P11405	helicobacte
145	6	1.2	171	1	CYSE_HELPY	O06059	marinococcu
146	6	1.2	172	1	CYSE_HELPY	P05195	neurospora
147	6	1.2	172	1	ECTA_MARNA	P77789	escherichia
148	6	1.2	176	1	3DHQ_NEOCR	O980j7	sulfolobus
149	6	1.2	176	1	YDES_ECOLI		
150	6	1.2	178	1	RL10_SULSO		

ALIGNMENTS

RESULT 1
EPA3_HUMAN STANDARD; PRT; 238 AA.
AC P52797;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Ephrin-A3 precursor (EPH-related receptor tyrosine kinase ligand 3)
DE (EFK-3) (EHK1 ligand) (EHK1-L).
GN EFNA3 OR EPFG3 OR LERK3 OR EFL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9510419; PubMed=7838529;
RA Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
RA Teepe M., Lyman S.D., Stintz S., Fletcher F.A., Gayle R.B. III,
RA Cerretti D.P., Beckmann M.P.,
RT "Ligands for the receptor tyrosine kinases hek and elk: isolation of
RT cDNAs encoding a family of proteins."
Gene 10:299-306(1995).

RP SEQUENCE FROM N.A.
RX MEDLINE=95063919; PubMed=7973638;
RA Davis S., Gale N.W., Aldrich T.H., Maisompierre P.C., Lhotak V.,
RA Pawsan T., Goldfarb M., Yancopoulos G.D.,
RT "Ligands for EPH-related receptor tyrosine kinases that require
RT membrane attachment or clustering for activity."
Science 266:816-819(1994).
RL
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKELETAL MUSCLE, SPLEEN,
CC THYMUS, PROSTATE, TESTIS, OVARY, SMALL INTESTINE, AND PERIPHERAL
CC BLOOD LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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CC
DR EMBL; U14187; AAC50078.1; -
DR EMBL; L37360; AAA52368.1; -
DR MIM; 601381; -
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin.1.
DR PRINTS; PR01347; EPHRIN.
DR PRODOM; PD002533; Ephrin.
DR PROSITE; PS01299; EPHRIN.1.
KW Glycoprotein; GPI-anchor; signal.
FT SIGNAL 1 22
FT CHAIN 23 238
FT EPHRIN-A3.
FT CARBOHYD 38 38
FT CARBOHYD 67 67
FT CARBOHYD 100 100
FT CARBOHYD 171 174
FT CONFLICT 71 74
SQ SEQUENCE 238 AA; 26350 MW; 8EFD6AE8FE33FD6A CRC64;

Query Match 1.6%; Score 8; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 79 AGPFGGG 86
DB 75 AGPFGGG 82

RESULT 2
SUT1_YEAST STANDARD; PRT; 299 AA.
AC P53032;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Probable sterol carrier.
DE SUT1 OR YGL162W OR G1828.
GN Saccharomyces cerevisiae (Baker's yeast).
OS Eukaryota; Fungi; Ascomycota; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
OX [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 28383 / FL100;
RX MEDLINE=96084960; PubMed=7489925;
RA Bourot S., Karst F.,
RT "Isolation and characterization of the Saccharomyces cerevisiae SUT1
RL gene involved in sterol uptake."
Gene 165:97-102(1995).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96158061; PubMed=8585324;
RA James C.M., Indge K.J., Oliver S.G.,